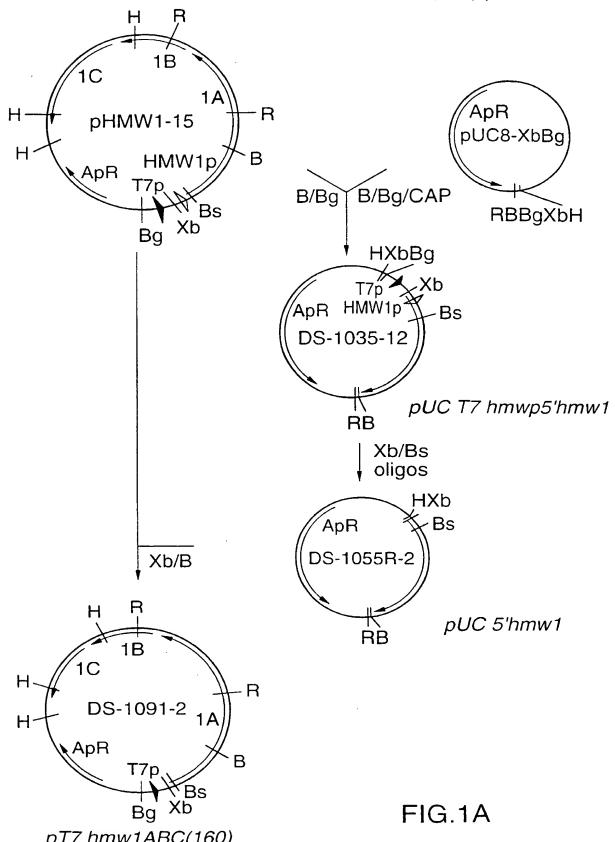
1/235

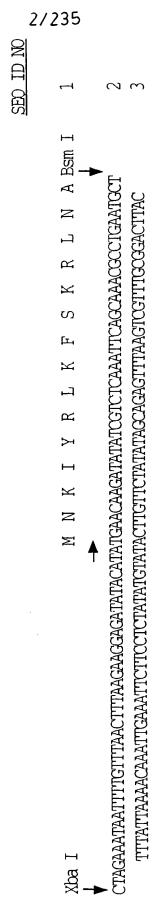
Construction of DS-1091-2,a hmw1ABC (160) plasmid.



pT7 hmw1ABC(160)

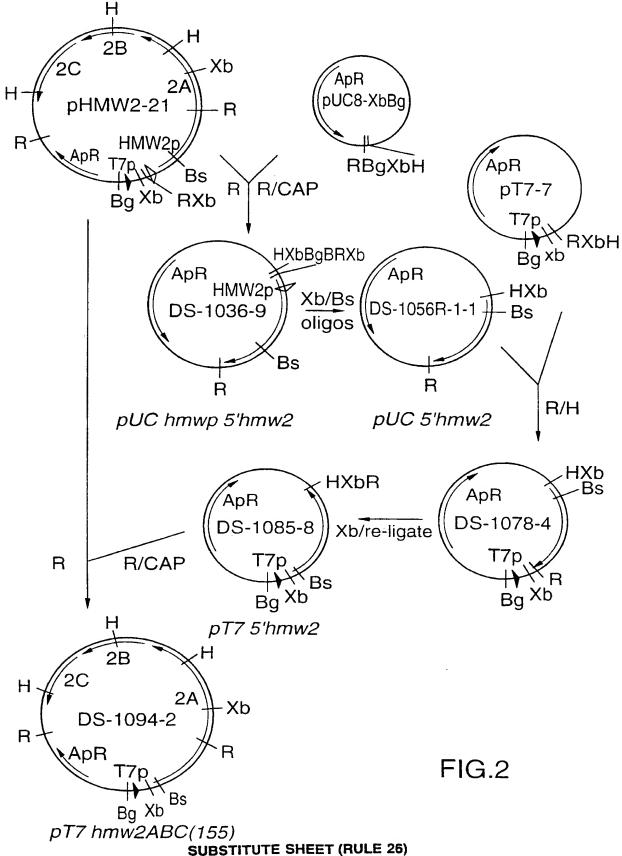
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Oligonucleotides to re-create the N-terminus of the full-length HMW1A protein in plasmid DS-1091-2 or the N-terminus of the full-length HMWZA protein in plasmid DS-1094-2



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Construction of DS-1094-2,a T7 hmw2ABC (155) plasmid.



Construction of DS-1046-1-1,a T7 hmw1ABC (125) plasmid.

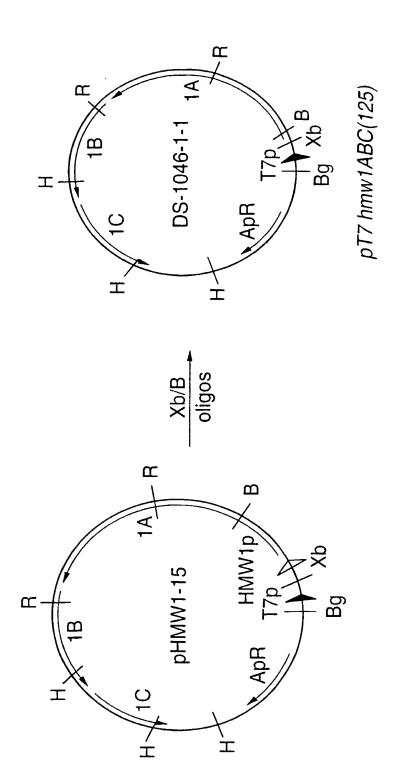
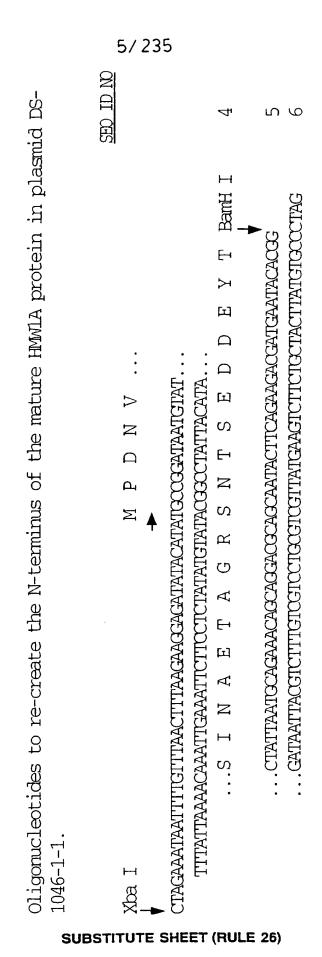
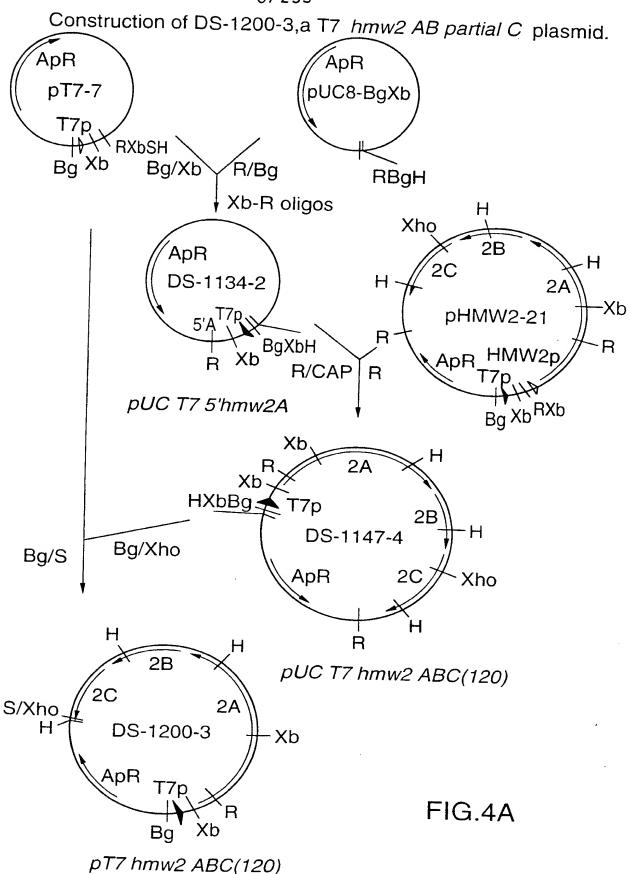


FIG.3A

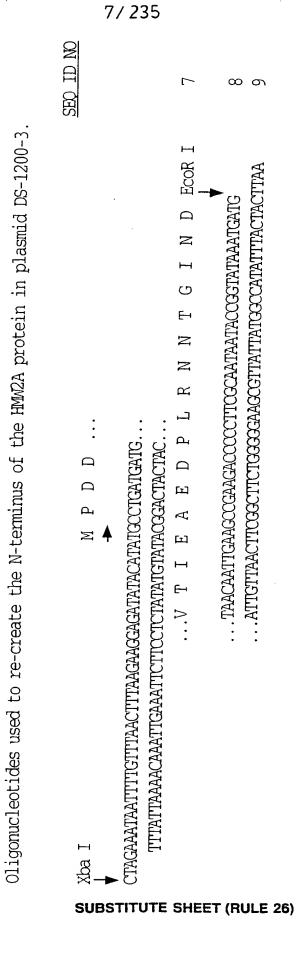


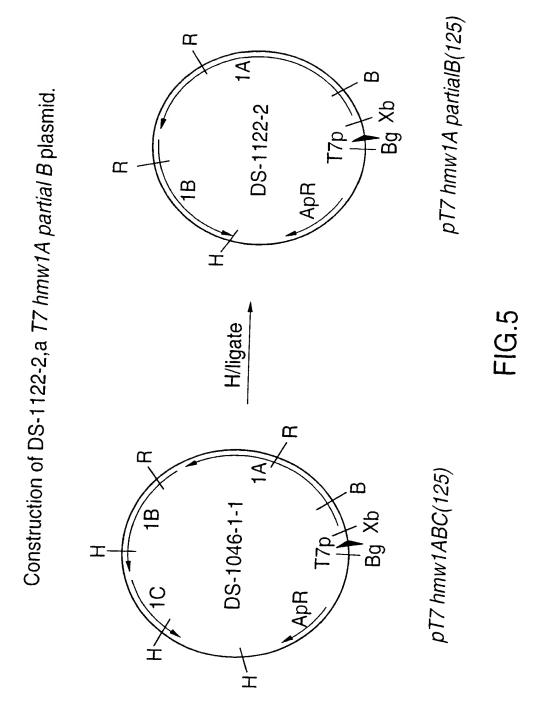




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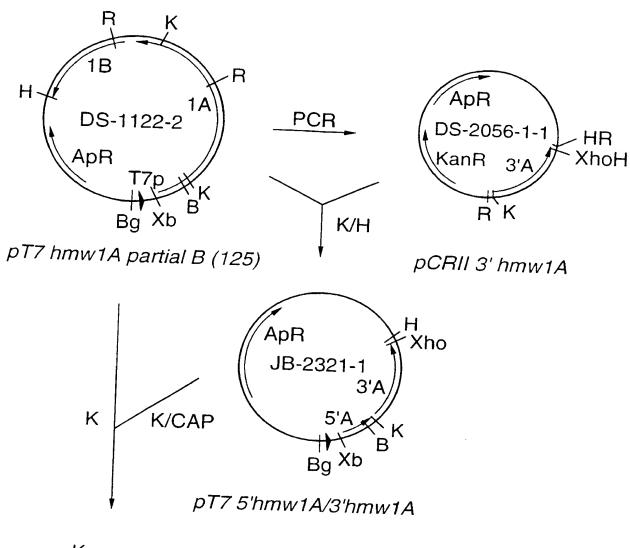
## FIG.4B





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9/235 Construction of JB-2330-7,a T7 hmw1A (125) plasmid.



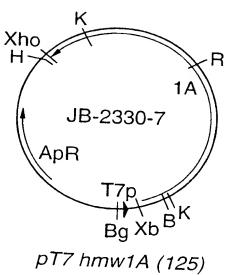
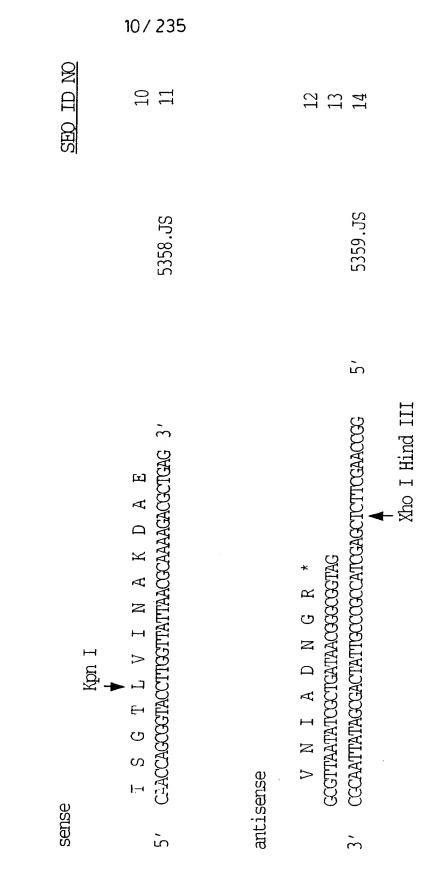


FIG.6A

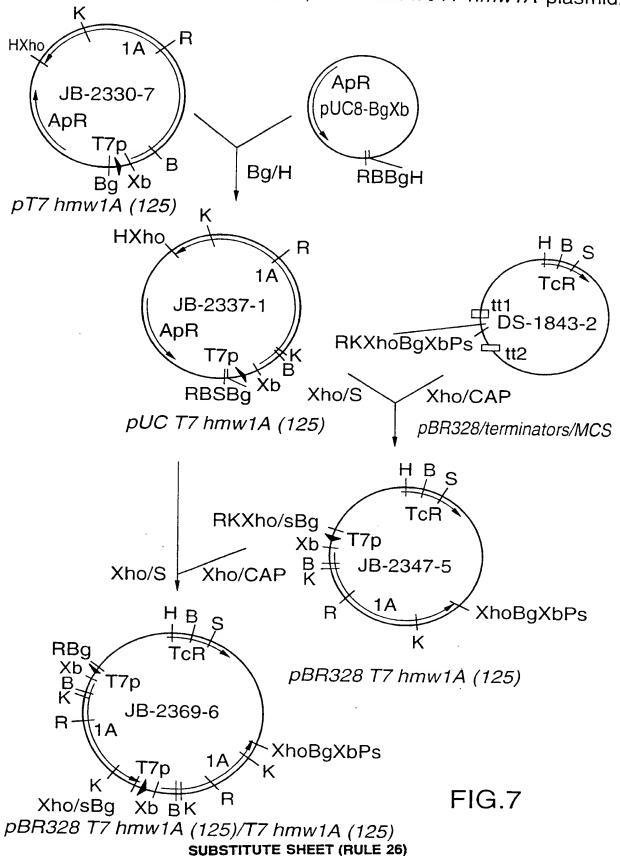
FIG.6B

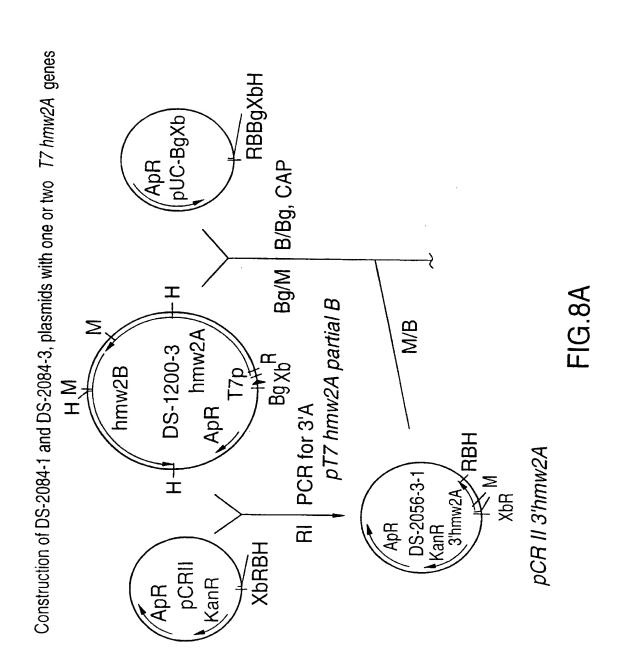
Oligonucleotides used to PCR amplify the 3'-end of hmwla.

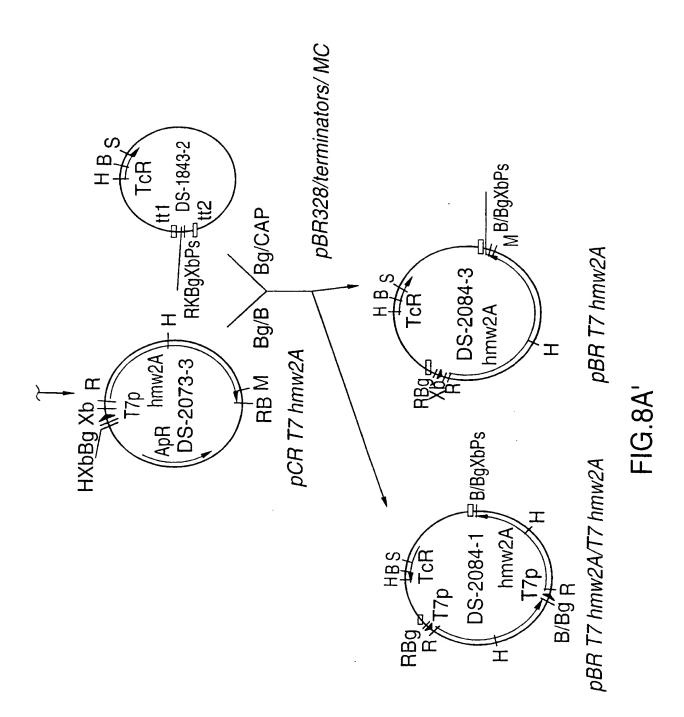


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Construction of JB-2369-6, a T7 hmw1A/T7 hmw1A plasmid.







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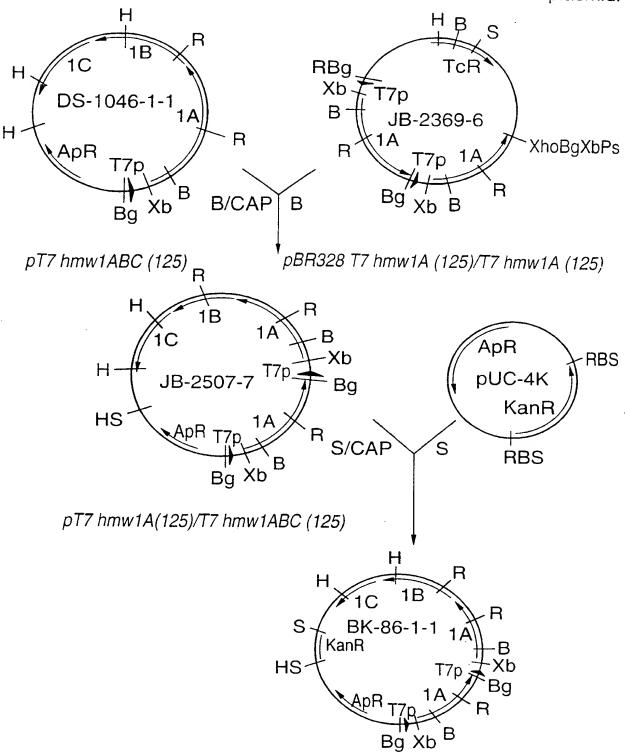
SEO ID NO 17 18 19 5360.DC Oligonucleotides used to PCR amplify the 3'-end of hmw2A. 2  $\overset{\cdot}{\sim}$ BamH I > × 口 П G > 24 О Ø EcoR I > Z antisense sense 2,

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FIG.8B

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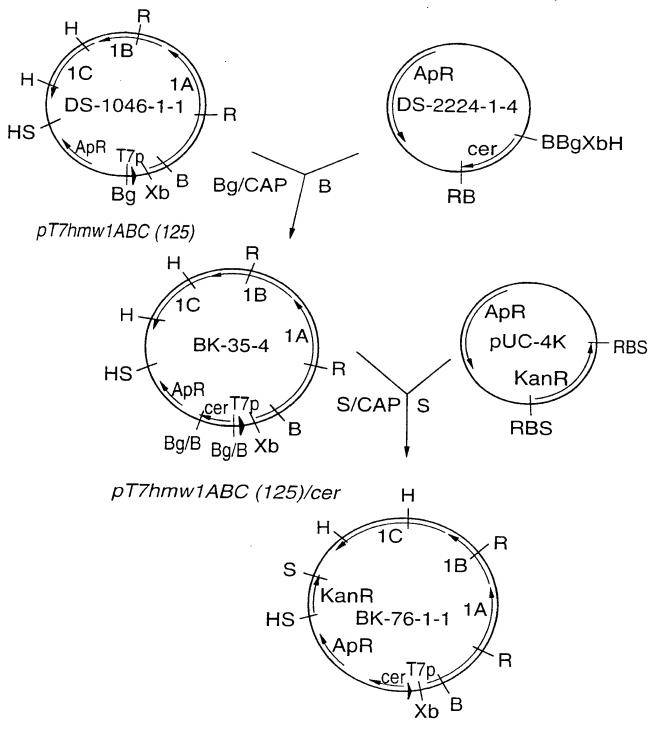
Construction of BK-86-1-1, a T7 hmw1A/T7 hmw1ABC/KanR plasmid.



pT7 hmw1A(125)/T7 hmw1ABC (125)/KanR

FIG.9
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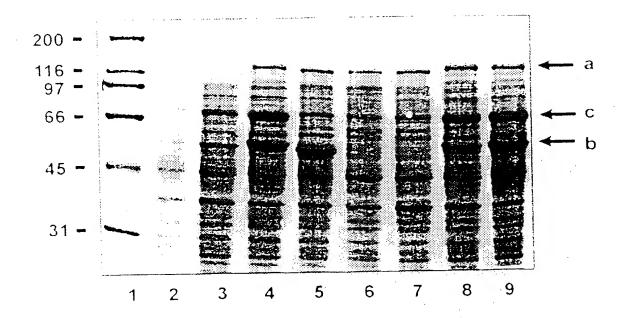
16/235 Construction of BK-76-1-1, a *T7 hmw1ABC/cer/KanR* plasmid.



pT7hmw1ABC (125)/cer/KanR

FIG.10

FIG. 11.



#### 18/235 Purification of rHMW1 from E.coli

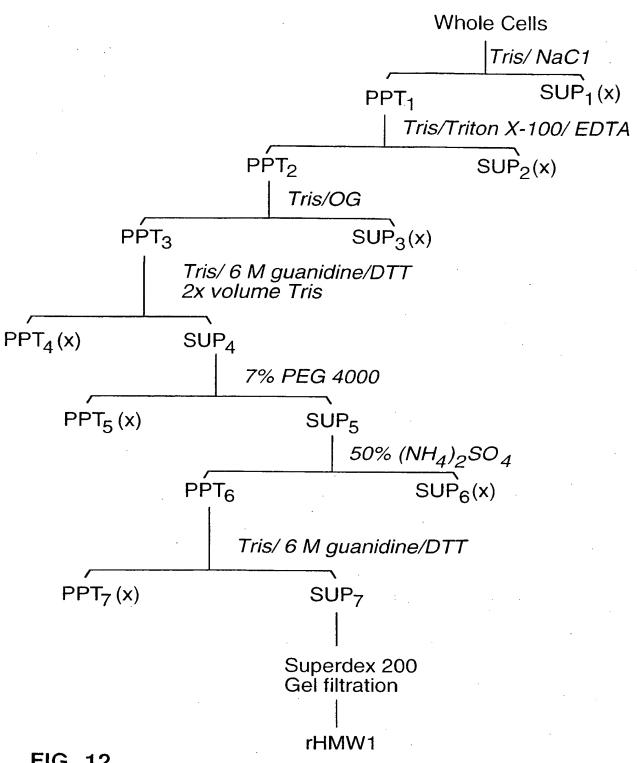


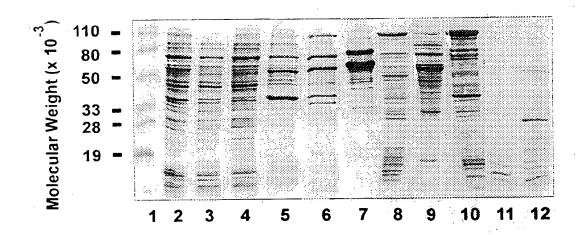
FIG. 12

All centrifugation is at 20,000g,30min. (x): to discard

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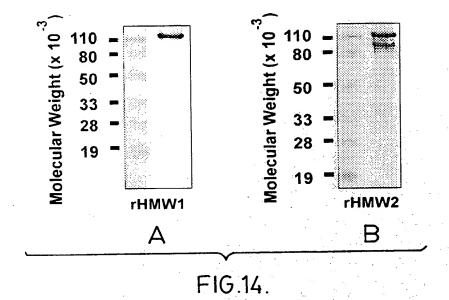
FIG.13.

### Extraction of rHMW1 from E. coli



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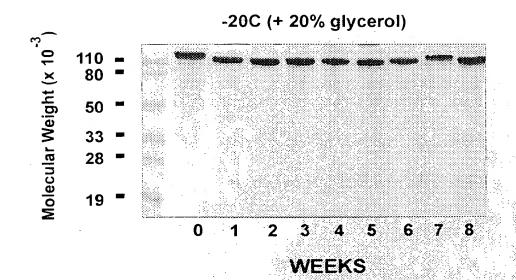
#### Purification of rHMWs from E. coli



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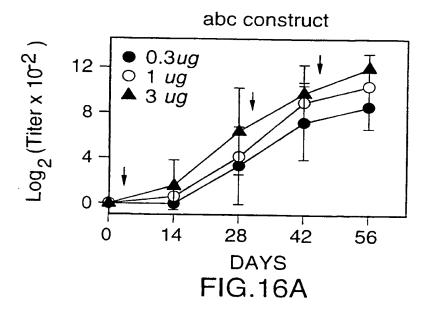
FIG.15.

The Stability of rHMW1 (abc/cer)



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#### Kinetics of Antibody Response to rHMW1 in Mice



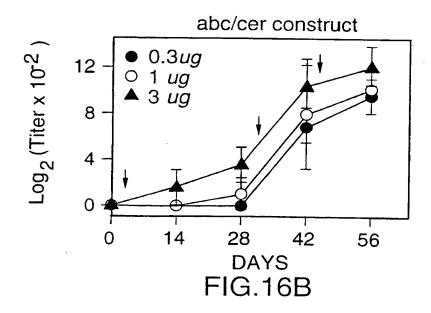


FIG. 17

Oligonucleotides used to PCR amplify hmwA genes from NTHi strains.

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VAL GLY 3 T C G G C I 10	GIN C A A	PHE T T T G	ALA GCTA
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# FIG. 18G

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	VAL THR PHI GTAACCTT 1930	ASN SER LY. AACAGTAA 1990	强
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GCAGCC

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, C A A A A T C 2290

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ASN A A T 2160	GLU G A A 2220	ILE A T C 2280
A SER GLU ASN G T C A G A A A T G 2130VAL THR THR LYS ALA GLY THR THR ILE ASN T T A C C A C C G G G C A C A T T A A T 2140 2150 2160	U VAL THR ALA A G T A A C A G C C A 2190 LYS THR GLY ASP ILE LYS GLY GLY ILE GLU A A A C A G G T G A A T T G A A 2200	N ILE THR ALA  TATTACAGCGA 2250 SER GLY ASP THR LEU ASN VAL SER ASN ILEGCGGCGACACGCTTAATGTAAGTAACATCGCGGCGACACGCTTAATGTAAGTAACATC
THR ACC	GLY GGA	LEU ASN VAL SER TTAATGTAAGTA 2270
THR CACA 2150	GLY A G G T 2210	VAL F G T A 2270
C G G C	LYS A A A	ASN A A T
ALA G C G	ILE A T T	LEU
ASN A A T G 2130 IHR LYS C C A A A 2140	 ASP G A T	N ILE THR ALA TATTACAGCGA 2250 SER GLY ASP THR GCGGCGACACGC
ASN A A T ( 2130 THR I A C C A 2140	ALA A G C C A 2190 GLY A G G T G 2200	ALA 1 G C G 7 2250 ASP 1 G A C A 2260
THR ALA SER GLU ASN C T G C G T C A G A A A T G 2120 2130VAL THR THR LYS T T A C C A C C A A A 2140	VAL GLU VAL THR ALA TAGAAGTAACAGCC 2180 2180LYS THR GLYAAACAGGTG	VAL ASN ILE THR ALA  3 T A A A T A T T A C A G C G A 2240 2250  SER GLY ASP THR G C G C G A C A C G
SER 3 T C ? VAL	VAL AGTA LYS AA	ILE LATI SER GC
ALA F G C C 2120	GLU A G A A 2180	ASN A A T 2240
THR	VAL	VAL
ILE LATC	SER	ASN A T
AL ASN F A A A 7 2110	LE GLY I A G G J 2170	R GLY CGG 1 2230
VAL A G T 7 22	ILE CATA	SER LTC (
LYS THR VAL ASN ILE THR ALA SER GLU ASN A A A C A G T A A A T A T C A C T G C G T C A G A A A T G  2110 2120 2130 VAL THR THR LYS  T T A C C A C A A A A A A A A A A A A A	ALA THR ILE GLY SER VAL GLU VAL THR ALA GCAACCATAGCGTAGCGTAGACTAACAGCCA 2170 2180 2190 LLYS THR GLY ASP AAACAGGTGAT	SER ASN SER GLY ASN VAL ASN ILE THR ALA  TCCAATTCCGGTAATGTAAATATTACAGCGA 2250 2250 SER GLY ASP THRGCGGCGACACG
LYS A A A	ALA G C D	SER T C (
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SER T C A 2340	GLY G G C 2400	VAL G T A 2460	THR ACA 2520
GLY GGA	ASN A A T	ASN A A T	THRACC
LYS A A A G	ILE A T T	LEU	THR
THR CACAA 2330	GLU FGAAA 2390	THR TACA ( 2450	ILE 2510
THR ACC 2	GLY G G T	ASN A A T A 24	ALA 3 C C A 25
THR ACAA	THR ACA(	G G C	GLY 3 G T (
VAL G T A A O	ASN 2370 HR LYS C C A A A A 2380	  SER A G C (	 A SER I C A G
SER GLY ALA VAL THR THR LYS GLY SERCAGGTGCCGTAACAACCACAAAAGGATCA 2320 2340	TGGTAATGCAAATA 2350 2360ILE THR THR LYS THR GLY GLU ILE ASN GLYTTACAACCAAACAGGTGAAATTAATGGCTTACAACCAAACAGGTGAAATTAATGGC	CGGTAATGTAAATA CGGTAATGTAAATA 2420ILE THR ALA SER GLY ASN THR LEU ASN VALTTACAGCGAGCAATACACTTAATGTA 2460	A A A T G T A A C A G T A A  2480 THR ALA ASN SER GLY ALA ILE THR THR THR  C A G C A A C T C A G G T G C C A T A A C A C A C A C C A C A C A C C A C A C C A C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C A C C C A C C C A C
G G T	ALA GCA THR ACA	ASN VAL A A T G T A LE THR T T A C A G	THR A C A ALA 3 C A A
SER	Y ASN TAAT TILE TAA	Y ASN TAAT ILE	N VAL TGTAP TGTAPTHR P
	GLY 1 G G T A 2360 I	GLY 2 G G T 1 2420 1	ASN A A T C 2480 T
		SER T C C	GIN C A A
	ALA THR THR SCAACAAC1	ALA G C T	GLY G G T
	SN ALA A T G C A 2350	SER TCA 10	THR ACT 70
	ASN A A T 23	LYS SI A A A T ( 2410	ILE T A T C A 2470
	THR ILE ASN ALA THR TH ACTATTAATGCAACAAC 2350	GLU VAL LYS SER ALA SER GAAGTTAAATCAGCTTCO	SER ASN ILE THR GLY GIN AGTAACATCACTGGTCA? 2470
	THRACT	GLU GAA	SER A G T

G A C A A C A G G T G G A C A A C A G G T G 2550 ASP ALA ASN ILE THR THR GLN THR GLY ASN A T G C A A A T A T T A C A A C C C A A A C G G T A A T 2580	CAGTTCTGGTT 2610  SER VAL THR LEU ILE ALA THR GLY GLN THR CTGTGACGCTTATTGCAACTGGACAAACT CTGTGACGCTTATTGCAACTGGACAAACT	R GLY ASP THR AGGTGACACTG 2670VAL THR ILE THR ALA ASP LYS GLY LYS LEUTACCATTACTGCGGATAAAGGTAAATTATACCATTACTGCGGATAAAGGTAAATTA	
THR ILE ASN ALACTATTAACGC	ILE ASN GLY LYS VAL GLU SER SER GLY A T T A A T G G T A A A G T T G A A T C C A G T T C T G G T T 2590 2600 C.SER VAL THR LEU C T G T G A C G C T T A A C T T A A C T T A A C C C T T A C A C	LEU ALA VAL GLY ASN ILE SER GLY ASP THR C T T G C T G T A A T A T T T C A G G T G A C A C T G 2650 2650VAL THR ILE THR 2680 2680	THR THR GLN THR SER SER LYS ILE ASN GLY ACCACACAAACAAGCTCTAAGATTAACGGAA 2710 2720
GLU GLY SER GAAGGCTCAA 2530	ILE ASN G ATTAATG	LEU ALA V CTTGCTG	THR THR GLN ACCACACAAA 2710

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37/235		
LEU T T G 2820	ALA G C A 2880	ASP 3 A T 2940
SER A G C	SER A G C	THR ASP
GLY G G T	THR ACA	ASN A T A
THR A C C 810	VAL G T A 870	ALA G C A A 2930
ALA G C G 2	ASN A A T	THR CAG
SER A G T	ALA G C T	VAL TTA
T A 0 VAL G T T	 0 GLU G A G	R ILE SER GLY AATCTCTGGCA 2910 ASN THR VAL ASN VAL THR ALA ASNASN THR VAL ASN THR ALA ASNATACAGTAAATGTTACAGCAAATA
ASN T A A ' 279 SER A G C 28	ALA A G C , 285 GLY G G T 28	THR ILE SER GLY A C A A T C T C T G G C A 2900 2900 ASN THR VAL ASNAT A C A G T A A A T C 2920
GLY FGG' VAL GTA	GLU FGA, THR ACA	SER TCT THR
SER LTC' THR CG	ILE A A T ' LYS A A	THR ILE C A A T C 00ASNA T A
ILE 1 A T 7 2780	LY. . A A 22840	THR A C A 2900 
		GLY GLY GCGGT
G G C	G G C	G G C
SER A G T 70	ALA G C A 30	11.E A T T (90
ILE ATT 27	GIN C A A 28.	THR A C A A C 2890
ASP G A T	THR ACT	THR GLY THR ILE CAGGTACAATT 2890
G G T	THR A C C	THR GLY THR ILE GLY GLY A C A G G T A C A A T T G G C G G T 2890
	TTCTGGTAATA  2790 THR VAL SER VAL SER ALA THR GLY SER LEUCGGTAAGCGTTAGTGCGACCGGTAGCTTG	A T T T C T G G T A A T A  2780  2780  2790  THR VAL SER VAL SER ALA THR GLY SER LEU  C G T A G C G T T A G T G C G A C C G G T A G C T T G  2820  A A A A A T T G A A G C A A  2840  2850  A A A A C A G G T G A G C T A A T G T A A C A A G C C A  A A A C A G G T G A G C T A A T G T A A C A A G C C A  A A A C A G G T G A G C T A A T G T A A C A A G C G C A  A A A C A G G T G A G C T A A T G T A A C A A G C G C A  A A A C A G G T G A G C T A A T G T A A C A A G C G C A  A A A C A G G T G A G C T A A T G T A A C A A G C G C A  A A A C A G G T G A G C T A A T G T A A C A A G C G C A  A B A C A G G T G A G C T A A T G T A A C A A G C G C A  A A B C A G G T G A G C T A A T G T A A C A A G C G C A  A A B C A G G T G A G C T A A T G T A A C A A G C G C A  A B A C A G G T G A G C T A A T G T A A C A A G C G C A  A B A C A G G T G A G C T A A T G T A A C A A G C G C A  A B A C A G G T G A G C T A A T G T A A C A A G C G C A  A B A C A G G T G A G C T A A T G T A A C A A G C G C A  A B A C A G G T G A G C T A A T G T A A C A A G C G C A  A B A C A G G T G A G C T A A T G T A A C A A G C G C A  A B A C A G G T G A G C T A A T G T A A C A A G C G C A  A B A C A G G T G A G C T A A T G T A A C A A G C G C A  A B A C A G G T G A G C T A A T G T A A C A A G C G C A  A A C A G G T G A G C T A A T G T A A C A A G C C C A  A A C A G G T G A G C T A A T G T A A C A A G C C C A  A A C A G G T G A G C T A A T G T A A C A A G C C C A  A A C A G G T G A G C T A A T G T A A C A G C C C A A C C C C A A C C C C

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THR A C C 3000	GLN C A G 3060	THR A.C A 3120	
LEU TTA	GLY G G T	VAL G T G	
THR ACT	ASN A A T	ASN A A T	
VAL F G T G 2990	SER A A G C 3050	ALA C G C C 3110	
ALA G C T	THR SER SER ASN GLY ACCTCAAGCAATGGT 3050	ALA G C C	
GLY GGA	THR A C C	ASN A A T	
2970 LYS ALA THR GLY GLY ALA VAL THR LEU THR A A G C A A C G G G G G G C T G T G A C T T T A A C C 2990 3000	A A C C A C C G A A A C A A  3020 3020SER SER ASP ILE THR SER SER ASN GLY GIN 3040 3040 3050	GGATAGCAGTATCG 3090 3080ALA GLY SER ILE ASN ALA ALA ASN VAL THRCAGGAAGCATCAATGCCGCCAATGTGA.CA 3120	LEU THR THR VAL   T T T A A C T A C T G T G G   3140
2970 THR . A C G (	A A C A A 3030 ASP 3040	TATC (3090 SER 3100	T G T G (
ALA GCA	CGA CGA SER	CAGT GLY GGAZ	t TR TAC
IYS ALA	THR THR GLU CCACCGAAA 20SER SER A	ASP SER 3 A T A G C A 80AIA G C A G	LEU ASN THR THR GLY THR LEU THR THR VAL TAAATACCACAGGCACTTTAACTACTGTGG 3130
	TF A A C 3020	3080 3080	R LEU TTTA 3140
	. T.	C A A	. 引 C A C
	THR FAC	ALA 3 G C	GLY A G G
2950	N GLY 3010	THR CAC (3070	IR THR CCAC 3130
53	GLY . G G A	LEU CTC 30	THR 'AC(
	ALA THR GLY GLY THR LEUGCAACAGGAGGTACTTT.	THR THR LEU THR ALA LYS ACAACTCTCACGGCCAA 3070	LEU ASN THR THR GLY THE TTAAATACCACAGGCAC 3130
	ALA G C A	THR A C A	LEU TTA

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GLY	THR	ARG	GLY
G G C	A C A	A G A	3 G T
3180	3240	3300	3360
ALA GLY SER LYS ILE GLU ALA ALA SER GLYCAGGTTCAAAAATCGAGGCAGCCAGTGGC 3160 3170 3180	S ASP ALA GIN A G A T G C T C A G T 3210 LEU ASP GLY ALA ALA LEU GLY ASP ARG THRTGGACGCGCGCATTAGGTGACCGTACA 3220 3230 3240	A ASN GLY SER A A A T G G C T C C G 3270 GLY SER VAL ILE ALA THR SER SER ARG G C A G C G T A A T C G C G A C A A C C T C A A G C A G A 3300	U ILE THR ILE AATCACAATAA 3330ASN GLY LEU ASN ILE ILE SER LYS ASN GLYASN GATTAAATATCATTTCAAAAAACGGT
ALA	ASP	SER	LYS
G C C	G A C C	T C A A	A A A
J ALA	GLY	A A C C 3290	SER
G G C A	A G G T		T T C A
3170	3230		3350
GLU GAG	ALA LEU GLY 3 C A T T A G G T C 3230	ALA THR THR SCGACAACCT 3290	ILE &
ILE	ALA	ALA	A ASN ILE
A T C	G C A	G C G	
LYS A A A A	LYS ASP ALA GIN A A A A G A T G C T C A G T 3200 3210LEU ASP GLY ALA T G G A C G C G C G C G C G C G C G C G C	GLU VAL ASN VAL THR ASN ALA ASN GLY SER GAAGTAAATGTAACTAACGCAAATGGCTCCG 3250 3250GLY SER VAL ILEGCAGCGTAATCC	VAL ASN ILE THR GLY ASP LEU ILE THR ILE G T G A A C A T C A C A C A T A A 3310 3320 ASN GLY LEU ASN A T G G A T T A A T A A T A A A T
SER I	T C A G '3210 GLY '3220 3220	ALA ASN GLY SER C A A A T G G C T C C C 3270 60GLY SER VAL G C A G C G T A A 3280	LEU ILE THR ILE  TAATCACAATAA 3330 20ASN GLY LEU ASNATGGATTAAAT
GLY G G T	ALA T G C ASP G A C	GLY TGGC' SER '	THR CAC GLY GGA
ALA GLY C A G G T T	LYS ASP ALA A A G A T G C 7 00LEU ASP T G G A C	A ASN CAAAT GLY GCA	U ILE THR AATCACAASN GLYATGGAT
: : :	LYS A A A A A 3200	C G C AZ 3260	TTTA 3320
	ASN ALA	ASN	ASP
	ATGCA	A A C	G A T
	ASN A A T	THR ACTA	G G G
	ILE	VAL	THR
	A T T A	GTA	ACT
	30	SO	0
	VAL ]	ASN V	ILE 7
	G T T A	A A T G	A T C A
	3190	3250	3310
	THR LEU VAL ILE ASN ALA	GLU VAL ASN VAL	VAL ASN ILE THR GLY
	ACCCTGGTTATTAATGC?	A A G T A A A T G T A A	TGAACATCACTGGG
	3190	3250	3310
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3420	3480	3540	
PRO GLY	ASP LEU	ARG PHE ILE GLU SGTTTTATTGAGC 3530	
PRO	ASP	ILE	
C C G	G A T	A T T	
: GLN	VAL LYS	PHE	
T C A A	3 T G A A A C	T T T T	
3410	3470	3530	
ILE	VAL	ARG	
A T T	G T G	C G T	
TYR	LYS	VAL	
. T A C	A A A	GTA	
TGTTAAAGGTGTTGAAA 3380 3390 ILE ASP VAL LYS TYR ILE GIN PRO GLY ILETTGATGTGAAATACATTCAACCGGGCATA 3400 3410	GLU VAL ILE GLU ALA LYS A A G T A A T T G A A G C A A A C 3440 3440ARG ALA LEU GLU LYS VAL LYS ASP LEU SERG C G C T C T T G A G A A G G A A T T T A T C T 3460 3470	GLU ALA LEU ALA LYS LEU A A G C A T T A G C T T G 3500 3510GLY VAL SER ALA VAL ARG PHE ILE GLU PRO G T G T G A G C G C T G T T T T A T T G A G C C A 3540	THR VAL ASP THR GIN ASN ACAGTCGATACACAAATG 3560 3570
AAAACACCGTGCTGT	ALA SER VAL TYR GLU 'G C G A G C G T A T A T G A A G 3430	ASP GLU GLU ARG GLU AG A T G A A G A A A G A G A A G A A G A A G A A G A A G A A G A G A A G A G A A G A G A A G A G A A G A G A A G A G A A G A G A A G A G A A G A G A A G A G A A G A G A A G A G A A G A G A A G A G A A G A G A A G A G A A G A G A A G A G A G A A G	ASN ASN THR ILE THR A A A T A A T A C A G 3550

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ILE	АТА	3600				ASN	A C A G T G A T G G C G C G A C G G T G T G C G T T A A T	3660				
ARG	C G A					VAL	GTT					
SE	AGT					CYS	TGC					
LEU	TTA	3590				VAL	GTG	3650				
PRO	CCA	m				選	ACG	m				
GLU PHE ALA THR ARG PRO LEU SER ARG ILE	A A T T T G C A A C C A G A C C A T T A A G T C G A A T A					ASN SER ASP GLY ALA THR VAL CYS VAL ASN	B D B					
黑	ACC	0	•	A	:	GLY	0 G C	0:				
ALA	GCA	3580	SER	3 G G C G T G T T T C T C A A	3630	ASP	GAT	3640				
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GLU.	. A A	•	CYS	T G 1		ASN.	. A C					
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			ARG	A G G			-		í í	AKG	555	
			GLY	0 0 0					;	ZTS CTS	999	
			CLU	GAA	3610				8	ASIN	AAC	3670
			SER	TCI	36				6	ASP	GAT	36
			VAL ILE SER GLU GLY ARG ALA CYS PHE SER	GTGATTCTGAAGGCA(					,	ILE ALA ASP ASN GLY AKG ***	ATCGCTGATAACGGCGGTAG	
			VAL	GTG						H	ATC	

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LEU ASP PRO ASP ASN VAL	30	SER ILE GLU ASN PRO SER THR GLU ARG ASN	TCCATTGAAAATCCTTCAACTGAACGCAAT	40 50 60	ASP LEU GLU TYR THR GLY	GACCTAGAGTATACAGGA 80 90	THR GLY GLU ASN ILE ASN ASN PRO LYS VAL	A C A G G G A A A A T'A A A C A A C C C T'A A G G T'A 110 110	011	LYS LYS THR LEU THR SER	AAAAAACACTAACAAGC	140 150	SER ILE LEU GLU ASN ILE LEU LYS GLY	TCAATCCTTGAGAACATCCTGAAAAAGGC	150 170 180
₫:		SER	JCC.		ASP SER ASN GLU ASP LEU GLU TYR	GATTCCAATGAAGACCTAGAGTAT 70	邢 …	A C A	•		4	130 140	SES	TCA	:

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GLY	ASN	ILE	
G G A	A A T	A T T	
240	300	360	
ASN ILE GLY	ILE	ASP	
ACATCGG	A T T	GATA	
ASN	LYS	VAL	
A A C	A A G A	G T T G	
ILE	VAL	TRP	
A T C A	G T T A	T G G	
230	290	350	
SER	GLY	GLY	
TCTA	G G T Q	G G A	
SER	GLY	LYS	
'AGCT	G G C G	A A A	
TGCCACTGATAAC  TGCCACTGATAAC 200 200 ILE TYR VAL ASN SER SER ILE ASN ILE GLY ATCTACGTTAATAGCTCTATCAACATCGGA 220 220 220	ASP SER CLY HIS LEU ILE LEU SER CLY CLY GACAGTGGTCACTTAATTCTCTCAGGTGGA 270  250 CLY ARG ASN CLY CLY VAL LYS ILE ASN GCCAGGAACGGCGCGCGTGTTAAGATTAAT 280	GGGCGGAAGTTTA 330 320 320 THR ILE ASN SER LYS GLY TRP VAL ASP ILE ACCATTAATTCCAAAGGATGGGTTGATATT 340 350	1 GLY THR GLY PHE TGGTACGGGTTTT 380 390
ASP GATA TYR TACG	GLY GGT ARG AGG	SER AGT ILE ATT	GLY GGT
ALA THR  GCCACTG  200  ALCT  ATCT	SER TCA GLY GGC	GLY GLY G C G G A P 20 THR A C C A	GLY THR GLY GTACGGGT 80
ALA 200 200 J	LEU 260 260	GLY 320 320 	GLY . G. G. T 380
	ILE A A T T	(Y.	-
SER PHE VAL ASN ILE THR TCTTTTGTTAACATTAC1 190	HIS LEU ILE ACTTAAT	LYS ASN ILE THR SER TH AAAATATTACTTCCAC 310	HIS SER ASN ILLE SER LET CACTCCAATATTTCACT 370
T A A C	/ HIS	Е ТНК	N ILE
	T C A (	ТАСТТ	TATTI
	250	310	370
VAL	GLY	ILE	ASN
FGTTP	T G G T C	LATTA	SAATA
190	250	310	370
PHE I T T T (	SER	ASN A A A T A	SER
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	44/235		
ALA	GLN	ASN	ASP
G C T	C A A	A A T	3 A T
420	480	540	600
VAL	ALA	LEU	PHE ASP
G T G (	G C A	T T A	TTCGAT
SER	VAL	SER LEU	LYS
T C C G	G T C (	TCTTTA	A A A T
GLY	ILE	VAL	HIS
G G T T	A T T G	G T G 1	CATA
410	470	530	590
ASN	GLN	ASN	THRACTO
A A T G	C A A	A A T G	
LEU ASN ILE THR SER ASN GLY SER VAL ALA TTGAACATTACCTCTAATGGTTCCGTGGCT 400	LYS ALA ARG A A G G C A C G T 450 SER ALA ALA ASP ALA GIN ILE VAL ALA GIN A G C G C A G A T G C T C A A A T T G T C G C A C A A 480	GLU ASN LYS GAAAACAAA 510 THR PHE ARG LEU ASN ASN VAL ACCTTTAGGCTTAACAATGTG 520	ILE THR SER ATCACGTCA 570 ASN VAL GLY ASN GLN THR HIS LYS AATGTGGCAATCAAACTCATAAA 580 590
THR TACCT	ARG C G T 450 ALA ASP C A G A T (460	  LEU C T T ?	SER F C A 570 GLY ASN GCAAT(
ILE A T T A 400	ARG C G T 450 ALA AS G C A G A	LYS A A A 510 ARG LA A G G C 5	SER T C A 570 GLY ASG G C A A
ASN A A C A	ASP LYS ALA ARG G A T A A G G C A C G T 440 SER ALA ALA AS A G C G C G C A G A	GLY GLU ASN LYS G G G A A A A C A A A 500 THR PHE ARG LI A C C T T T A G G C 5	SER II.E THR SER T C C A T C A C G T C A 560 570 ASN VAL GLY AS A A T G T G G C C A A 580
	LYS AAGC SER	GLY GLU GGGAAA 00 THR ACCT	ILE ATCA ASN VAATG
: : :		GLY G G G G 500	
	LYS	THR	LEU
	A A A	A C A	CTA
	ASP	ASN LEU	GLY
	G A C	ACCTCP	G G T
	3 ALA	2 ASN	VAL GLY GIN GLY
	G G C A	A A A C	STGGGTCAAGGTC
	430	490	550
	LYS A A G	ILE 'ATA 4	GLY G G T 5
	PHE GLU LYS ALA ASP LYS	GLY ILE ILE ASN LEU THR	GLY VAL GLY GLN GLY LEU
	TTTGAGAAGGCAGACAAA	GGCATCATAAACCTCACA	GGAGTGGTCAAGGTCTA
	430	490	550
	PHE T T T	G G C	GLY G G A C

C T T 780

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ALA	$G \subset A$	099		
扭	GCACCTGCGACAACCGCA			
TH	ACA			
ALA	S C G	.650		
PRO	$C \subset T$			
ALA	GCA			

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AACGGC... ASIN TTT T T C 阳阳 GTA WAL 000 GLY CCGGA GLY SER ₽ AGC 贸

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	46/235		
GLY G G A 840	PRO C C T 900	ASP G A T 960	SER T C T 1020
VAL GLY GTCGG 84	LYS A A G	PHETTT	ILE A T C
ASN A A C G	SER AGCA	SER TCTT	ASN A A T A
LEU CTTA 830	ASN A A C A 890	VAL G T G T 950	ILE A A T T A 1010
VAL GTG(	ASN A C A 8	SER TCTG	THR ACAA 10
MET A T G	THR ACA?	GLY G G C 1	ASN A A C A
THR ASN GLY ASN MET VAL LEU ASN VAL GLY A C G A A T G G C A T G G T G C T T A A C G T C G G A 820 840	GTTTAATTTGAAG  GTTTAATTTGAAG  870  PRO ASN GLU ASN THR ASN ASN SER LYS PRO CCAAATGAGAATACAAACAAGCCT CCAAATGAGAATACAAACAAGCAAGOCT CCAAATGAGAATACAAACAACAGCAAGOOT	CGCCAATATTACA 920 920 ALA ILE GIY GLY SER VAL SER PHE ASP GCCATTGGTGTGAG950 940	CGGCAGAGGGCT CGGCAGAGGGCT 980 GLU LEU LYS MET ASN THR ILE ASN ILE SER GAATTAAAATGAACACAATTAATCTCT 1000 1020
A	THR ASN SER ARG VAL LEU PHE A CTAATTCGAGAGTTTTGTTT 860 850	LEU PRO LEU GIN PHE ASN ALA TTACCGCTTCAATTTAACGCC? 920 920 G	ILE HIS ALA ASN HIS SER GLY A T A C A C C C A A T C A T C C G G C P 970 G

ASP GLY THR SER LEU THR LEU GIN SER HIS GACGGCACCAGCCTCACCTACAATCCCAT 1030 1040 1050 VAL ARG LYS ASP SER ALA PHE ILE ILE SER GTTCGCAAAGATAGTGCTTTTATAATCAGT 1080	IXS ASP LEU THR ILE ASN ALA THR GLY SER A A A G A T T T A A C G C A A C C G G T T C A  1100  1110 ASN PHE THR LEU GLU GLN SER PRO ASP SER A A T T T T A C T C T G A G C A A C C A G A C A G T 1140	PHE THR ASP LYS TYR PRO GLY ARG ALA ILE  T T T A C T G A C A A G A G C T A T T  1150  SER SER THR LYS ASN ILE THR ILE SER GLY  A G T T C A A C T A A A A A A A C C A T C T C	GLY ASN VAL SER LEU GLY GLY GIN ASN SER GGCAACGTCTCTTGGTGGGCAAATTCA 1210 1220 1230
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1LE A T C 1260	ARG A G A 1320	ALA G C G 1380	GLU G A A 1440
THR ACCA	SER T C C A	VAL GTT	SER A G T
ILE A T T A	ALA G C T T	SER T C A G	THR ACCA
ASN A A A T A 1250	PHE 7 T T T C 1310	THR GLY 1 C C G G C 7	GLU A G A G P 1430
GLY GGA	ASP GACT	THRACC	GLY GGAG
SER SER ASP ILE LYS GLY ASN ILE THR ILE A G C A G T G A C A T C A A G G G A A A T A T T A C C A T C 1260	THR LEU LYS ALA CACTGAAAGCC 30 HIS ASN SER PRO ARG ASP PHE ALA SER ARG CATAACAGCCTCGCGACTTGCTTCCAGA 1300 1320	TGAATGTTGAA  TGAATGTTGAA 10 1350 GLY ASN LEU THR LEU THR GLY SER VAL ALA GGAAATTTAACCCTAACCGGCTCAGTTGCG	SER ILE LEU ASN  C C A T T C T T A A C  1410  ASP ALA THR PHE LYS GLY GLU THR SER GLU  G A T G C T A C T T T T A A G G A G A C C A G T G A A G C A G T G A A G C A G T G A A G C A G T G A A G C A G T G A A G C A G T G A A G C A G T G A A G C A G T G A A G C A G T G A A G C A G T G A A G C A G T G A A G C A G T G A A G C A G T G A A G C A G T G A A G C A G T G A A G C A G T G A A G C A G A C C A G T G A A G C A G A G A C C A G T G A A C C A G T G A A G C A G A G A C C A G T G A A C C A G T G A A C C A G T G A C C A G T G A A C C A G T G A A C C A G T G A A C C A G T G A A C C A G T G A C A C A C A C A C A C A C A C A C A
SP ILE ACATC 1240	ALA 5 C C 1290 SER PRO 1300	GLU 1 A A 1350 JEU THR T A A C C 1360	ASN 1 A C 1410 THR PHE C T T T T 1420
ASP GAC 12	THR LEU LYS ALA TACACTGAAAGCC 1280 1290 HIS ASN SER PICATAACAGCC	C T T G A A T G T T G A A  1340  GLY ASN LEU TF  G G A A T T T A A C 1360	LEU ASN C T T A A C 1410 ALA THR PH G C T A C T T T
SER	THR LEU LYS CACTGAAAG 80 HIS ASN \$ CATAACA	LEU ASN VAL TGAATGTT 40 GLY ASN GGAAAT	SER ILE LEU CCATTCTT? 00 ASP ALA GATGCTA
SER AGCA	THR LEU CACTG 80 HIS CAT	LEU ASN T G A A T ( 10 G G A A	CATT CATT ASP GAT(
	T A 128	C T 134	T T 1.74(
	VAL TGT	LEU GLY ASN TTGGCAA(	ASN LEU
	ASN A A A T G	GLY	ASN FAA
	R THR : A A C A A 1270	IR LEU	LYS GLY AAGGTP 1390
	SER T C A A 1270	THR A C C C 1330	LYS A A A 13
	LYS SER SER THR ASN VAN AAAAGCTCAACAAATGT 1270	THR LEU THR LEU GLY ASIACCT TGGCAA 1330	ASP ILE LYS GLY ASN LEG SATATTAAAGGTAACCT 1390
	LYS A A A A	THR A C C	ASP 3 A T A

T T A 1620

AT

FIG. 19H

G Ø Ø GGA Ø, GLY Z Ø 0 6 6 ⊟ CATTASIN GLY A A 1490 GAA ₽ 日日 ASIN Ø ΑT Ø TTA AAC ں ASN ASP E C C G A ⊱ ⊱ IER GEZ 000 T G G  $\mathcal{O}$ A A C... ACCAAT... A C C... Ø 1600 GCTGAA. Æ GLY . ე AC K GGC ⊱ E-E æ ALA AT AT A A AA TC Н AAT. E AACAATAAT GGA E 出 田田 ASIN ASN ASIN CAAGGTAA ⊢ AA Ø AAC AAAACC ASIN ASIN 開 GLY ် ဗ GLY GEN LYS ASIN G AGT CAA  $\mathcal{O}$ GIN HH 開 SER CAØ ⊢ ⊱ ں ASN ASP ASIN Ø Ø A. ACA G G AACA Ø Ø ASN LYS ASN WAL Ø Ø Z, G CAA Ø G 园 GIN WAL AT  $\circ$ G AAC A C <u>ე</u>  $\mathcal{O}$ ASIN ASIN

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A A

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CA

A A

	7	
GIN	CAA	
SE	$T \subset G$	
띰	A T C	1670
ASIN	AAT	$\leftarrow$
GLY	C G C	
GLY	$\mathcal{C} \mathcal{C}$	00
H	ATT	1660

CAA

			ILE	ATC	
			THE	ATCAATATTACCAAGAAGATAACAATC	
			ILE	A T A	1730
			LYS	A A G	<b>~</b>
			LYS	A A G	
		:	TH	ACC	0
IXS	ACAATTCTTCTGATAAA	1710	ILE THR	ATT	1720
ASP	GAT		ILE ASN	AAT	
SE	TCT		田田	ATC	
SER	$T \subset T$	1700	:	:	:
THR ILE	A T T	<b>,</b>			
開	ACA				
国	$\mathcal{O}$	0			
ASN	AATCT	1690			
GLY	$\mathcal{O}$				
LYS	AAAGG				

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LYS A A A 1740

	ILE	AGCCCAGCAAGTAATGCTAATCTAACCATT	1800	
	混	ACC		
	LEU	C T A		
	ASN LEU	AAT	1790	
	ALA	G C T	<u></u>	
	ASN	AAT		
:	SER	AGT	000	
1770	ALA SER	GCA	1780	
	PRO	CCA		
	SER	AGC		
1760	:	:	•	
1750				

G G T GLY

G G T

GAA BB

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			CIN	GAA	1860
			ALA	$G \subset E$	
			PHE ASN LYS ALA GLU	AAA	
			ASIN	AAT	1850
			盟	TTT	$\overline{}$
			CILY	CTAAATATTTCAGGCTTTAATAAAGC£GAA	
•	•	:	SER	$T \subset A$	0
ASP	GAC	1830	ILE	ATT	1840
GLU LEU THR GLY ASP	GAATTAACAGGAGAC		LEU ASN	AAT	
開	ACA		邑	СТА	
LEU	TTA	1820	:	:	:
CLU	GAA				
TEO T	C T A				
開	ACG	10			
LYS	AAA	1810			
開	ACCAAAACGCT				
IYS	AAA				

#### FIG. 19.

GAT

ASN A A C (

AATGGC

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ATTACAGCT

ILE

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ASN A A T 1920	ASN A A T 1980	ASN A A T 2040	
ASP GLY ASN ALA SATGGTAATGCT? 1910	HIS C A C A	SER AGT?	
ASN A A T	GY GGT	ASP GAT?	
GLY : G G T 1910	. ASN T A A C 1970	ALA ASP 5 C T G A T G 2030	
ASP G A T	SER ALA ASN GLY CAGCTAACGGTC	ALA G C T	
SER AGTG	SER T C A	SER AGT(	
30 ILE GLY LYS ALA SER ASP GLY ASN ALA ASN A T T G G C A A G G C T A G T G A T G G T A A T G C T A A T A T T G G C A A G G C T A G T G A T G C T A A T T A T G C T A A T G T A A T G T A A T G T A A T G T A A T	F ASP LYS VAL LYS  TGACAAGGTTAAA  1940  ASP SER LYS ILE SER ALA ASN GLY HIS ASN  GATTCAAAATCTCAGCTAACGGTCACAAT  1960  1970	S VAL GLU THR SER AGTGGAAACGTCT 2000 ASN SER ASP SER SER ALA ASP ASP SER ASN AATAGTGATAGTAGTAAT 2020 2040	THR ILE SER ALA AACCATTTCCGCA 2060 2070
G G C	ASP LYS VAL 3 A C A A G G T T A 40 ASP SER G A T T C A A	AL GLU THR TGGAAACG 10 ASN SER AATAGT(	SER TCCG
ILE ATT (	LYS A A G ASP G A T	SER LYS VAL GLU GCAAAGTGGAAA 2000 ASN S	LEU THR ILE FTAACCATTT 2060
1880	ASP 7.G A C 1940 (	VAL 2000 2000	THR A A C C 2060
	THR PHE A C T T T T	LYS	LEU PTT/
	THR 3 A C T	SER I A G (	THR GLY ACTGGT1 )
1870	ALA LYS LYS VAL THR PH GCTAAAAAGTGACTTT 1930	VAL THR LEU ASN SER LY GTAACACTAAATAGCAA 1990	ASP ASN ASN THR GLY LE GATAACAACACTGGTTT 2050
<u>;;</u>	LYS A A A A A	LEU A C T 1	ASN CAA
	LYS F A A i	THR A A C .	ASP ASN ASN ATAACAACA 2050
	ALA G C .	VAL G T 7	ASP G A C

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THR A C C 2100	THR A C A 2160	GLY G G C 2220	SER A G C 2280
VAL G T C	SER AGCA	SER A G T	ALA G C A 7
ASP G A C G	LYS GLU A A A G A A A	ILE A T T	GLN C A A G
ASN S A A T G 2090	LYS C A A A 2150	ASP C G A T A 2210	THR 2270
ASN A A C 7	THR ACCA	GLY GL C C C 22	THR ACCA 22
VAL GTA	THR AACAA	THR AACA(	LEU CTTAA
LYS ASP VAL THR VAL ASN ASN ASP VAL THR A A A G A T G T A A A C A A T G A C G T C A C C 2080 2100	ILE SER ALA THR  TCTCTGCCACA 2130  THR GLY ASN VAL THR THR LYS GLU SER THR ACAGGAAATGTAACAACCAAAGAAAGCACA 2160	LY SER VAL GLU GTAGCGTGGAA 10 2190 VAL THR ALA LYS THR GLY ASP ILE SER GLY GTAACTGCTAAAACAGGCGATATTAGTGGC	ASN VAL THR A A T G T T A C A 2250 ALA THR ASP SER LEU THR THR GIN ALA SER G C A A C T G A T A G C T T A A C C C C A A G C A C C A 2280
VAL I G T A 7 2080	C A C A 2130 ASN A A A T G 2140	GGA 219 219 ALA TGC	TACA 2250 ASP TGATA
ASP AGATO	SER ALA FCTGCCA THR GLY	CGTGC CGTGC AACTC	ASN VAL A A T G T T I ALA THR S C A A C T G
LYS A A A (	ILE SER ALA LA TCTCTGCC 2 2120 THR GLY ACAGGAP	GLY SER VAL GTAGCGTG 80 VAL THR GTAACTC	VAL ASI, T A A A A A A A A A A A A A A A A A A
: : :	N ILE TAT 2120	R GLY 2180 2180	IR VAL 2240 2240
	LE AS	A TH	TE NE
	HR II	LA AI	LY ASGTA
	SER HIS LYS THR ILE ASN CCCACAAGACAATAAA 2110	THR ILE ASN ALA ALA THR CCATTAATGCGGCCACi 2170	THR ILE SER GLY ASN THR CAATTTCTGGTAATAC <i>i</i> 2230
	HIS LACA	ILE A TTA	TTT T
	SER HIS LYS THR ILE ASN ILE SER ALA THR TCCCACAAGACAATAAATATCTCTGCCACA 2130 2110 THR GLY ASN VZ	THR ILE ASN ALA ALA THR GLY SER VAL GLU ACCATTAATGCGGCCACAGGTAGCGTGGAA 2170 2180 VAL THR ALA LY 2200	THR ILE SER GLY ASN THR VAL ASN VAL THR ACAATTCTGGTAATACAGTAAATGTTACA 2250 2230 ALA THR ASP SE GCAACTGATAC 2260
	<b>-</b>	. 4	•

#### FIG. 19L

SER SER ILE THR SER SER ASN GLY GLN THR  TCTAGCATTACCTCAAGTAATGGTCAGACA  2290  2310  THR LEU THR ALA LYS ASN GLY SER ILE  ACTCTTACAGCCAAGAATGGCAGTATCG  ACTCTTACAGCCAAGAATGGCAGTATCG  2320  2320  2320  2330  2350  2350  2350  2370	ASN THR SATACCA  AATACCA  SER GLY  CAGTGGCA	2420 2430 LEU ALA ILE ASN ALA LYS ASP ALA LYS LEU TTAGCTATTAACGCAAAGATGCTAATTA TTAGCTATTAACGCAAAAGATGCTAACTAA 2460	ASP GLY THR ALA SER GLY ASP ARG THR VAL GATGGTACTGCATCAGTGACCGCACAGTA 2470 2480 2490
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FIG. 19M

L 0	r E OS	5 <del>L</del> O	, E S
GLY G G T 2520	ASN A A T 2580	ILE A T T 2640	ARG C G T
SER I C I (	ILE A T A	GLU G A A	LYS A A G
GLY 3 G C '	THR ACAA	ALA 3 C T (	ALA 3 C G J
SER GLY A G T G G C T 2510	SER A A G C A 2570	LYS GLY ALA A A G G T G C T C 2630	ILE GLU ALA TTGAAGCGP
ALA GCAP 25	LEU S	LYS , A A G 26	ILE TTG
VAL ASN ALA THR ASN ALA SER GLY SER GLY GTAAATGCAACTAACGCAAGTGGCTCTGGT 2520	SER SER ASN VAL CAAGTAACGTG 40 ASN ILE THR GLY ASP LEU SER THR ILE ASN AATATCACTGGAGATTTAAGCACAATAAAT AATATCACTGGAGATTTAAGCACAATAAAT	AS ASN GLY LYS  A A A A T G G T A A A  2610  ASN THR VAL VAL LEU LYS GLY ALA GLU ILE A A C A C C G T A G T G T T A A A A G G T G C T G A A T T 2620  2640	RO GLY VAL ALA CAGGTGTAGCA 50 2670 SER ALA ASN GLU VAL ILE GLU ALA LYS ARG AGTGCGAATGAGGTTATTGAAGCGAAGCGT
ALA THR CAACTA 2500	  GLY 3 G A G	LYS A A A 2610 VAL VAL 3 T A G T G T	ALA 3 C A 2670 ASN GLU A T G A G G
ALA 13 C A A 2500	VAL G T G 2550 THR GLY A C T G G A 0	LYS A A A 2610 VAL VA 3 T A G T	GIN PRO GLY VAL ALA CAACCAGGTGTAGCA 2660 2670 SER ALA ASN GL AGTGCGAATGA
ASN A A T G	ASN A A C ( ILE A T C A	ASN GLY A A T G G T A ASN THR	VAL GTA ALA GCGA
VAL GTAA	SER AGTA ASN AATA	ASN A A T ASN A A C	GLY GGT( SER AGTG
: : :	SER T C A A 2540 A	LYS 3 A A A A 2 2600 A	PRO A C C A ( 2660 
	THR ACCT	SER T C G A	GIN C A A
	ALA G C A	ILE A T T	ILE A T T
	ALA G C G G 30	ILE ATC 90	TYR TATA 50
	VAL THR PSTG TG 2530	ASN ] AATA 2590	LYS A A A T. 2650
	SER VAL THR ALA ALA THR SER SER ASN VAL A G T G A C C T C A G T A A C G T G 2550 2530 2540 ASN ILE THR GI 2560	GLY LEU ASN ILE ILE SER LYS ASN GLY LYS GGATTAAATATCATTTCGAAAATGGTAAA 2590 2610 ASN THR VAL VP 2620 ASN THR VAL VP	ASP VAL LYS TYR ILE GATGTGAAATATATT 2650
	SER A G T G	GLY G G A	ASP GAT

### FIG. 19N

	55 / 235	
GLY G G T 2760	GLU G A A 2820	SER A G T 2880
LEU	ASN A A T	SER TCAA
ALA LYS LEU SCTAAACTT 950	GIN C A A	PHE T T C T
ALA A G C T 2750	THR 7 A C A 2810	ALA CYS ; C G T G T T 2870
THR LEU	ASN A A T	ALA G C G
THR	VAL G T C	LYS A A G G
A G A T T T A T C T G A T  2720  2720  GLU GLU ARG GLU THR LEU ALA LYS LEU GLY  G A A G A A A C A T T A G C T A A C T T G G T  2760  2760	TGTTGAGCCAAAT 2780 2780 ASN THR ILE THR VAL ASN THR GIN ASN GLU AATACAATTACAGTCAATACACAAAATGAA 2820	A A G T C A A G T G A C A  2840  ILE SER GLU ASP LYS ALA CYS PHE SER SER  A T T T C T G A A G A C A A G C C T G T T T C T C A A G T  A T T T C T G A A G A C A A G C C T G T T T C T C A A G T  A T T T C T G A A G A C A A G C C T G T T T C T C A A G T  A T T T C T G A A G A C A A G C C T G T T T C T C A A G T  2860
S	T G 278	2 84 284 284
ALA LEU GLU LYS VAL LYS GCCCTTGAAAAGTAAA 2710	VAL SER ALA VAL ARG PHIGTA GTA GTGCTGTA CGTTT 2770	PHE THR THR ARG PRO SER TTTACAACCAGACCGTC. 2830

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ASIN GCAGTATGT VAL GGTAATGGTGCA 2890 ALA ASIN

THR ASP ASP ARG GIN CTGACGATAGACAG

Ø

G A T A G A C 2920

K1 hmw1A sequence

FIG.20A

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Ø Ø ⊱ ACC ARG ASIN A A GGA AAA AAC. GLY LYS TAT CI AGA 国 ARG GCA AA TCAAATTAAC ALA ASIN ⋖ C C C A. PRO IE IEI E-E AACAATGAGTACGAC... ACAACA... TGCA TA ALA GE A A 160 ASIN ASIN E ... TCTATTAA ... TCGCCAAA A G ASIN A A GAG RS GEU GACCCGGAT CTAACAAAC ASP SE ... C T T LEI SE PR0 ASIN E AAT ACA Ø ASN B THE G CCCA ⊱ 国 贸 AAG G R 园 A C GAG <u>Г</u> CCATCC GAG AAA

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SER HIS LED THR LED TRP SER GLV GLY ASP SER ASP TILE ASN TILE GLY ASP SER CCCACTTAGGAGACAGC  GTTAATAGTGATATCAATATTGGAGACAGC 220 220 220 220 220 220 220 220 220 22	TCAATATTGGAGACAGC  TCAATATTGGAGACAGC 240 230 TTAATGTTACAGGCAAT 290 300 310 SLY TRP VAL ASP SER GATGGTTACAGGCAAT 350 350
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THE CLU ASP ILE THR THR LYS GLN GLY ASP ILE ALA  A00  THE GLU ASP LYS PRO GLY LEU SER ASN LEU  TTCGAAGACAACCAGGGCTGAGCAACCTA	430 440 THR ILE THR ALA LYS GLY THR ILE ALA VAL A C C A T T A C A G C T A A A G G G A C C A T T G C G T G A C C A T T A C A G C T A A A G G A C C A T T G C G T G A 60 470 480	ASN ASN LYS LYS GLY PHE ARG PHE ASP ASN A A C A A G A A A G G C T T T A G G T T T G A T A A T  490 VAL THR LEU ASN GLY THR GLY GLY GLY LEU G T C A C T C T A A A T G G A G G A G G C T C 540	SER PHE LYS TYR ILE GLU THR GLY ASN ARG  TCTTTTAAATACATCGAAACCGGAAATAGA 570  ASP SER ASN PHE GLU THR HIS PHE ARG GLY GATAGCAATTCGAAACCCATTTTAGAGGA

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LEU

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<u>ပ</u> Ø 0 G C  $\mathcal{O}$ Ø ASN Ø G B Ø GAG. GIN GGCGCT650 CAG GEN WAL G G TCTTCCCT ARG ASIN PR0 A G AA TGGAAT... G G C... A T C... Ø, CGATTG E 段 CAAG 640 ARG AGT Ø G ATG ACC ... A G T G C C 閨 G T A CGCTCCCAC TTGATAGC EEG. T T A ... G T A WAL 段 AAA G G G ARG ILE Ø TCA G G A ₽ 段 GLY AC ⊱ CACTGG ں CGT Ø ⊣ ASIN ASIN K Ø Ø K AGA Ø ARG 图 AGA S S S <del>[--</del> ARG ARG T T

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CAGT

AAC 099

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TRP

980

970

-1G.20E

PHE ASN ASN ASP THR VAL PHE ASN ILE ALA TTTAATAATGACACTGTTTTAATTGCA 820 830 840	ALA SER SER ALA VAL ASN PHE ASN ILE LYS GCAAGTTCGGCGGTTAACTTTAACATCAAA 850 PRO PRO ILE VAL ASP LYS VAL THR ASN GLY CCACCAATAGTAGACAAAGTAACCAACGGG CCACCAATAGTAGACAAAGTAACCAACGGG	HIS THR LEU PHE LYS GLY ASN ILE SER	AATCACACATTATTCAAAGGGAATATTTCA 930 VAL LEU GLY GLY MET SER THR PHE ILE GTTTTAGGGGGGGGATGTCAACTTCATT 940	HE ASN ALA SER SER ASN TYR GLN THR TTAACGCCTCCTCCAGCAACTACCAGACTT
	ALA SER S CAAGTT	ASN HIS T	ATCACA	HE ASN ALA TTAACGC
	O		H	T; F-

	r.	4	
S r A 020	T אן 180	AL A F T G 1140	G
PHE :	PHE 7 T T A 1080	AL T T 11	ILU A 2
_ L		P 5	ب ر
ASN A A	ALA G C	GIN C A .	田田
LN A A	D C	SIN A C (	¥
G (	A S C	A 4	A C
SER T C A 1010	HIS C A C 1070	SER LEU ASN GLN VAL A CATTGAACCAAGTTG 1130	ILE A T A
LU A G	H.	E C	
. G V	T T	85 1	AS A
ILE A T A	  SER J C G	  ILE A T A	  LYS
E I I	C A. 050. 17 3 T '	C A. 110. EN	. C. C. L70.
I. 3 A 2	PHE 1 1 1 GI GI GI 106(	ALA 3 C ( 1, 1, AS AS 1120	SER 15 17 A A A
VAL G T (	XS A A A GLU G A A	SN A T ( GLY G G (	YS A A A ALA 3 C C
G C -	A A A B C C C C	A A A L	L L L L L L L L L L L L L L L L L L L
. G G	LEU LT. SI SI		LYS A A A II II A T
TYR	ER 3 C 7 040 LYS A 7	E 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 C 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	SE 10 10 10 10 10 10 10 10 10 10 10 10 10	11 T T T T T T T T T T T T T T T T T T	H L T : :
	SER I C A	LEU PTA	ASN 1 A T
	B B B	A G	SI A (
	GLY G G 7 030	ASN A A 7 090	ASP G A T 150
	説 C A 1	YS A A 1	LE T T
	U	IAA	I A
	ALA G C	ILE	GLY 3 G C
	E C	(A Z )	A C
TYR GLY VAL ILE ILE GLU SER GIN ASN PHE S ATGGCGTGATTATAGAGTCACAAACTTAA 1000 1010 1020	ER ALA SER GLY GER SER LEU LYS PHE  G T G C C T C A G G T C A A G C T T A A A T T C A  1030 LYS SER GLU GLY SER THR HIS ALA ALA PHE TA A A G C G A A G G T T C G A C A C G C C G C T T T T A 1080	HR ILE LYS ASN ASP LEU ILE LEU ASN ALA  CAATAAAAATGATTTAATTTTAATGCCA  1090 THR GLY GLY ASN ILE SER LEU ASN GLN VAL AND THE CAATGAACCAAGTTG GGGGGAATTGAAGTTG AND THE CAATGAACCAAGTTG GGGGGGAATAATATCATTGAACCAAGTTG GGGGGGGAATATATCATTGAACCAAGTTG AND THE CAATGAACCAAGTTG GAACCAAGTTG GAACAAGTTG GAACCAAGTTG GAACAAGTTG GAACCAAGTTG GAACAAGTTG GAACAAGTTG GAACAAGTTG GAACAAGTTG GAACAAGTTG GAACCAAGTTG GAACAAGTTG GAACAAAAAAAAAA	LA GLY ILE ASP SER ASN LEU LYS LYS SER CAGGTATTGATAGTAATCTCAAAAAAGCC 1170 1150LEU ILE ALA ASN LYS ASN ILE THR PHE GLU G

A C C 1400

LY GLY ASN ILE THR LEU ALA ALA ASP LYS  GGGCAATATCACCCTTGCAGCCGATAAA 1230  1210 LYS PRO ILE GLU ILE LYS GLY ASN ILE THR VAACCAATAGAAATCAAAGGTAATATTACTGAACCAATAGAAATCAAAGGTAATTACTG	AL LYS GLU GLY ALA ASN VAL THR LEU ARG  TTAAAGAAGCCAATGTCACCCTTCGTA 1290  1270 SER ALA ASN TYR GLY ASN ASP LYS SER ALA LGCGCGAATTATGGTAATGACAAATCAGCTT 1320	EU SER ILE ARG GLY ASN VAL THR ASN LYS  TAAGTATAAGAGGAAATGTCACTAATAAG  1350  1330 GLY ASN LEU THR VAL THR GLY SER ALA ILE A GLY ASN LEU THR VAL THR GLY SER ALA ILE A GCAATCTCACGTTACGGCTCGGTATCA  1380	SN ILE GLU LYS ASN LEU THR VAL GLU GLY A T A T A G A A A A A A T C T T A C C G T T G A A G G T A
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YR S A C A 1440	.S G 1 G G 1500	A G 60	HA
TYR T A C _ 144	LYS G A A G G 1500	SER 7 I C C G 1560	ASN I
ASN	ALA 3 C T P	LYS A A A T	ASP LEU ATTTAP
A A		T H	I I
PRO C C A A	ILE A T C G	THR ACTA	ASP G A
ALA ASN CTAATC 1430	SER T C C A 1490	THR A C C A 1550	LYS GLY
SER ALA LYS PHE LEU ALA ASN PRO ASN TYR 3GTGCTAAGTTTTTAGCTAATCCAAATTACA	LEU PHE ASP ASN CTATTTGACAACC 1460 1.460GIN GLY LYS SER ASN ILE SER ILE AIA LYS CAAGGCAAGTCAAACATTTCCATCGCTAAGG	TE	
LEU FTA	 A A C A	  ASN	ARG
ALA LYS PHE LEU CTAAGTTTTTAG 1420	LEU PHE ASP ASN CTATTGACAACC 1460 1GIN GLY LYS SER ASNAAGGCAAGTCAAACA	LYS ASP ILE GLU ASN A A G A T A T C G A G A A T A 1520 1530THR GLY SER LEU AS C T G G C A G T C T G A A	THR ILE ILE LYS GLY  CTATTATAAAGGGTA 1580 1590ASN ILE THR ASN ARG
S G T 14	AS A P P P P P P P P P P P P P P P P P P	ASA A A A A A A A A A A A A A A A A A A	GLY G G T 151 X AST T A A
LY. A A	ASP 3 A C A LYS 1 A A C	SEU SEE AGAG	A G THE
ALA G C T	PHE 7 GLY GLY G G C	ILE GLU TCGAGI GLY SER	LE LYS TAAAG( ILE THR
는 단 (2	A A A	I A O O O T O T O T O T O T O T O T O T O	I A J
G T C	LEU C T A T 1460 GIN A A	ASP G A T A 1520 THR C T	ILE II A T T A T 1580 ASN
	C C C C C C C C C C C C C C C C C C C	LYS A A A	THR ACT
	ER PHE ASN VAL SER GLY LEU PHE ASP ASN  GCTTTAACGTATCCGGCCTATTGACAACC 1450 1460 1470 GIN GLY LYS SER AAAGGCAAGTCAA	LY GLY ALA ILE PHE 1 GAGGAGCTATTTTA 1510	SP SER ASN HIS HIS ACT CCAACCATA 1570
	ER PHE ASN VAL SER GCTTTAACGTATCC 1450	ILE A T T T 1510	HIS HIS CCACCAT 1570
	A C (	ALA C T ? 15	SER ASN CCAACC 15
	T A	A G	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \
	T T T	LY GLY ALA GAGGAGCT 1	SER T C (
	現 5 こ	LY G A	SP A C T

FIG.20

LE THR ASN ASN GLY ASP ASN THR GLU ILE  T C A C G A A T A T A C T G A A A T C C  1630  1GIN ILE GLY GLY ASN ILE SER GLN LYS GLU G A A A T T G C C G C A A T A T C T C C C A A A A G A A G 1680	IY ASN LEU THR ILE SER SER ASP LYS VAL  GCAATCTCACAATTCTTCTGATAAGTCA  1690 1710  ASN ILE THR GLU ARG ILE THR IILE LYS ALA GCAGAGCGGATAACAATCAAAGCAG  1740 1720 1730 1740	LY VAL ASN GLY ASP ASN SER ASP SER ASN  G C G T T A A T G G G A T A A C T C T G A T T C A A A T G  1750 GLU ALA THR SER ALA ASN LEU THR ILE LYS TA G G C A A C A A G T G C T A A C C T A A A A A 1780  1790	HR LYS GLU LEU LYS LEU THR ASN ASP LEU CCAAAGAGTTAAAATTAACAAACGACCTAA 1810 1820 1830
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FIG.20.

	66/235		
ASN ILE SER GLY PHE ASN LYS ALA GLU ILE T A T A T T T C A G G T T T T A A T A A G C A G A A A T T A 1850 1860	HR ALA LYS ASP ASN SER ASN LEU THR ILE  C A G C T A A G A A A T T T A A C T A T T G  1880  1870 GLY ASP ASN SER ASP ALA GLY ASN THR ASP A  1920  1920	LA LYS LYS VAL THR PHE SER ASN VAL LYS  C T A A A A A G T A A C C T T T A G C A A T G T T A A A G  1930 ASP SER LYS ILE SER ALA SER ASP HIS ASN V ATTCAAAATCTCTGCTAGCGACCATAATG ATTCAAAAATCTCTGCTAGCGACCATAATG	AL THR LEU ASN SER LYS VAL GLU THR SER  TAACGCTAAACAGCAAACATCTG  2000  2010  1990 GLY ASP THR ASP SER THR GLU ASP GLY GLY A GCGATACTGACAGCACTGAAGATGGCGGCA  2020
	出 し	LA C T A	AL

20K

N ASN ASN THR GLY LEU THR ILLE THR ALA  2050 2070  2050LYS ASN VAL THR V. LYS ASN VAL THR V.  2080A A A A T G T A A C A G G C T C A C G G C T T A C T G C A A C A C A C A C A C A C A C A C A
A A C T A T T A C T G C A A  A A C T A T T A C T G C A A  2060  2070 LVS ASN VAL THR VAL ASN ASN ILE THR  A A A T G T A A C A G T A A C A A T A T T A C T T  T A T C A C T G C G T C A G  2120  2130  A A A T G T T A C C A C A A G C G G C A C A C C A A A C A C C A A A C A C C C A A A C A C C A A A C A C C C A A A C A C C C A A A C A C C C A A A C C C A A A C C C A A A C C C A A A C A C C C A A A C A C C C A A A C A C C C A A A C C C A A A C C C A A A C C C A A A C C C A A A C C C A A A C C C A A A C C C A A A C A C C C A A A C C C A A A C C C A A A C C C A A A C C C C A A A C C C C A A A C C C C A A A C C C C A A A C C C C A A A C C C A A A C C C C A A A C C C C A A A C C C C A A A C C C C A A A C C C C A A A C C C C A A A C C C C A A A C C C C A A A C C C C A A A C C C C A A A C C C C A A A C C C C A A A C C C C A A A C C C C A A A C C C C A A C C C C A A C C C C A A C
A A C T A T T A C T G C A A  2060  2070 LYS ASN VAL THR VAL A  A A A A T G T A A C A G T A A  T A T C A C T G C G T C A G  2120  2120  2130 GLU ASN VAL THR THR L  A A A A T G T A A C C A C C A  A A A A T G T A A C C A C C A  T A T C A C T G C G T C A G  2130  T A G C G T A G A G T A A  2180  SER VAL GLU VAL  T A G C G T A G A A G T A A  2180  2180  THR ALA LYS THR GLY A  2180  2180  THR ALA LYS THR GLY A  2280  C A G C C A A A C A G G T G A  ASN VAL ASN ILE  T A A T G T A A T T A  2240  2250

SUBSTITUTE SHEET (RULE 26)

THR ALA SER GLY ASP THR LEU ASN VAL SER ACAGCGAGCGACACGCTTAATGTAAGTA 2260 2270 2280	SN ILE THR GLY GIN ASN VAL THR VAL ALA ACATCACAGGTCAAAAGGTGACAGTGGCAG 2290 2310 ALA SER GLY ALA VAL THR THR LYS GGTGCCGTAACAAAGGGTGCCGTAACAAAAGGGTGCCGTAACAAAAGGGTGCCGTAACAAAAGGGTGCCGTAACAAAAGGGTGCCGTAACAAAAGGATGCCGTAACAAAAGGATGCCGTAACAAAAGGATGCCGTAACAAAAGGATGCCGTAACAAAAGGATGCCGTAACAAAAGGATGCCGTAACAAAAGGATGCCGTAACAAAAGGATGCCGTAACAAAAGGATGCCGTAACAAAAGGATGCCGTAACAAAAGGATGCCGTAACAAAAGGATGCCGTAACAAAAGGATGCCGTAACAAAAGGATGCCGTAACAAAAGGATGCCGTAACAAAAGGATGCCGTAACAAAAGAAGAAGAAGAAAGA	LY SER THR ILE ASN ALA THR THR GLY ASN GATCAACTATTAATGCAACAACTGGTAATG 2350 2350 2350ALA ASN ILE THR THR LYS THR GLY GLU ILE ACAAATATTACAACCAAAACAGGTGAAATTA 2400	SN GLY GLU VAL LYS SER ALA SER GLY ASN A T G G C A A G T T A A A T C A G C T T C C G G T A A T G  2410  2.410 VAL ASN ILE THR ALA SER GLY ASN THR LEU A TAAATTACAGCGAGCGCAATACACTTA  2460
	THR GLY GL ACAGGTCA 2290	TATTAA 2350	J VAL LY AGTTAA 2410
	SN ILE THI ACATCAC	LY SER THR GATCAACT	SN GLY GLU A T G G C G A A

GTA

AAT

GLN C A A

C C T

THR ACT

ILE A T C

AAC

SER AG

VAL G T A 69/235

# FIG.20M

		05/255		
2490	THR VAL THR ALA ASN SER GLY ALA ILE THR TCAGTAACAGCAAACTCAGGTGCCATAACAA	ILE ASN ALA THR A T T A A C G C G A C A A 2540 THR GLY ASP ALA ASN ILE THR THR GLN THR G C A G G T G A T G C A A A T A T T A C A A C C C A A A C A G C A G G T G A T G C A A A T A T T A C A A C C C A A A C A G	S VAL GLU SER SER AGTTGAATCCAGTT 2600 2610SER GLY SER VAL THR LEU ILE ALA THR GLY G CTGGTTCTGTGACGCTTATTGCAACTGGAC 2620 2630	<pre>LE SER GLY TTCAGGTG 2670</pre>
2480	C A (	ILE A T T A 2540 THR C A	VAL G T T G 2600 SER C T	ASN A A T A 2660
2470		HR THR GLU GLY SER THR ILLE ASN ALA THR  CCACAGAAGGCTCAACTATTAACGCGACAA 2550 2530THR GLY ASP ALA ASP ASP ASP ASP ALA ASP ASP ASP ASP ASP ASP ASP ASP ASP AS	LY ASN ILE ASN GLY LYS VAL GLU SER SER GTAATCCAGT 260 260 2590SER GLY SER VAICTGGTTCTGT 2600	IN THR LEU ALA VAL GLY ASN ILE SER GLY A A A C T C T G C T G T A G G T A A T A T T C A G G T G 2650 2670

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ACACTGTTACCATTACTGCGATAAGGTA 2690 2700	SER SER LYS ILE AGCTCTAAGATTA 2720ASN GLY THR LYS SER VAL THR THR SER SER GASN GLY THR LYS OF GTGTAACCACCTCAAGCCACGGAACTAAGAGTGTAACCACCTCAAGCCACGGAACTAAGAGTGTAACCACCTCAAGCC	ASP ILE SER GLY THR ILE SER GATATTAGTGCACACAATTTCTG 2790 GLY ASN THR VAL SER VAL SER ALA THR GLY SGTAATACGGTAAGCGTTAGTGCGACCGGTA 2820	THR GIN ALA GLY SER LYS ILE  ACTCAAGCAGGCTCAAAATTG 830 GLU ALA LYS THR GLY GLU ALA ASN VAL THR S AAGCAAAAACAGGTGAGGCTAATGTAACAA 2860 2870 2860
	YS LEU THR THR GIN THR AATTAACCACACAAACA 2710	IN SER GLY ASP ILE SER A A T C A G G T G A T A T T A G T 2770	ER LEU THR THR GLN ALA GCTTGACCACTCAAGCA 2830
	YS A	A	년 D

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GLY

ALA

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## FIG.200

# FIG.20P

	72/235		
SER ILE ALA GLY SER ILE ASN ALA ASN VGTATCGCAGGAAGCATCAATGCCGCCAATG 3120	AL THR LEU ASN THR THR GLY THR LEU THR  TGACATTAAATACCACAGGCACTTTAACTA 3150 3130THR VAL ALA GLY SER LYS ILE GLU ALA ALA SCTGTGGCAGGTTCAAAATCGAGGCAGCCA 3180	ER GLY THR LEU VAL ILE ASN ALA LYS ASP  G T G G C A C C C T G G T T A T T A A T G C A A A G A T G  3190  3200 Ala Gin Leu ASP GLY ALA ALA SER GLY ASP H C T C A G T T G G A C G G C G T G A C C 3240	IS THR VAL VAL ASN ALA THR ASN ALA ASN ACACAGTAGTAATGCAACCAACGCAAACG 3250GLY SER GLY SER VAL ILE ALA THR THR SER SGCTCCGGCAGCGTAATCGCGACAACCTCAA 3300

LEU

ASP

GLY

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ASIN

VAL

ER ARG

## FIG.20Q

	73/235		
GCAGAGTGAACATCACTGGGGATTTAATCA 3330 3310THR ILE ASN GLY LEU ASN ILE ILE SER LYS ACAATAAATGGATTAAATTCATTCAAAAA 3350	GLY LYS ASN THR VAL LEU LEU LYS GLY  GGTAAAAACACCGTGCTGTTAAAAGGTG 3370 3370VAL GLU ILE ASP VAL LYS TYR ILE GIN PRO GTGAAATTGATGTGAAATACATTCAACCGG	LY ILE ALA SER VAL ASN GLU VAL ILE GLU GCATAGCGAGCGTAAATTGAAG 3430 3.430ALA LYS ARG ALA LEU GLU LYS VAL LYS ASP LCGAAACGCCCTTGAGAAGTAAAGATT 3480	EU SER ASP GLU GLU ARG GLU THR LEU ALA TATCTGACGAAGAAACATTAGCTA 3490 3500 3510
ರ	N A C	C C	西日

	747 255		
LYS LEU GLY VAL SER ALA VAL ARG PHE ALA G A A C T T G G C G T G A G C G T T T T G C T G 3520 3530 3540	LU PRO ASN ALA ILE THR ILE ASN THR  A G C C A A T A A T G C C A T T A C G A T T A A T A C A C  3550  3550 GIN ASN GLU PHE THR THR ARG PRO LEU SER G  A A A A T G A G T T T A C A A C C A G A C C A T T A A G T C  3500	IN VAL THR ILE SER GLU GLY LYS VAL CYS A A G T G A C A A T T T C T G A G G T A G G T A T G T T 3630 3610PHE LEU ILE GLY ASN GLY ALA THR ILE CYS TT C T T A A T C G C C A A C A A T A T G C A 3660	HR ASN ILE ALA ASP ILE GLU ARG *** CCAATATTGCTGATATTGAGCGGTAG 3670 3680

FIG.21A

K21 hrm/1A sequence

A T A... ₽ ASP G A E ASP GACCCGGA R2 ASP Ø 园 L G 国 E E G ت ك A G G Ø AA ... ASN ILE VAL ASN GLY SER ASN ... A A T A T T G T C A A C G G A A G T A A T ...

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75/235

T G C T

G B

ATT

ILE

CAGCCAGGTAGAGGCGATACACCC...

ASP

GLY

ARG

GLY

PRO

GIN

B

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... ASN LYS VAL SER ALA GLU GLY LEU

T C

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TCCACCGCTTTA... TTA LEU CA 開 Ø ည ည ALA E G ASIN Ø Ø AC ASIN Z,  $\vdash$ Ø

140 150... ... GIN LYS GLY ILE GLU VAL ?

 $C \subset C$  $T \subset T$ ATT ILE AAC ASN GTC GAG ... CAAAAGGGTATT 160

: A T C A C C... 390...

AAC

ASN A A T 7 380

GAT

ILE THR
ATTACTT
370

ASN A A T

LEU TTG/

SER TCC

SAN ALA ASP VAL  C A A C G C G A T G T T  200  210  ASP VAL LYS ASN GLY THR LEU VAL LEU HIS  G A T G T T A A A A C G G A A C A T T A G T A T T A C A T  220  230  LYS ILE ASN GLY  ASN ILE THR SER THR GIN ASN GLY ASN LEU  ASN ILE THR SER THR GIN ASN GLY ASN LEU  ASN ILE THR SER THR GIN ASN GLY ASN LEU  AS T A T A T A C C T C A A C A A A T G G T A A T T A C C T C A A C A C A A A A T G G T A A T T T A C C T C A C A C A A A A T G G T A A T T T A C C T C A C C A C A A A A
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G.21C

IR A C C 420	SER T C T 480	LYS A A G 540	ASN A A C 600
ILE A T T A	VAL G T A 1	HIS CAT	HIS C A C
THR ACCA	ASN A A T	訊 A C C C	PRO
LEU CTAA 410	SER AGTA	HIS CATA	THR ACA( 590
ASN A A T (	PHE IT A	ASN AATC	THR THR
ASP 3 A T 2	ARG 1 G A T	GLY 3 G T A	GIN
PHE GLU LYS GLY ASP ASN LEU THR ILE THR TTTGAAAAGGTGATAATCTAACCATTACC 410	ASN ILE ILE SER ASN GLN GLU A A T A T A T C T C T A A T C A A G A G 440 ASN LYS GLN LEU A A T A A A C A A C T T P	MET GLY ALA GLY LEU THR PHE A T G G G G G G T T T A A C T T T T T T T T T T T T T T	PHE ASP GLY THR LEU ASN ILE SER GLY LYS  TTTGATGGCACGCTTAACATTTCCGGAAAG  550  VAL VAL ILE ASN GIN THR PRO HIS ASN GTAGTAATTAATCAAACCACACCTCACAAC
	GLY G G ?	GLY GGC	GLY GGC SE
	ALA GIN GLY CCCAAGGAA	LEU ASN GLY TAAATGGG7	ASP (GATG
	ALA G C C	LEU TTA	PHE T T T G

ALA

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720 GGT 099 ⊱ Ø Ø Ø 园 AA TAGCT (710) ⊱ G ALA MET ပ ď Ø  $C \perp T$ GAA LEG VAL GE 650 G ACT T G ΑT 段 ASIN Ø AGCAACCGC ⊢ Ę٠ ASN AC AA  $T \subset T...$ A A G... TGTA GGCAAG LYS 760 GAC 贸 GTA AA AAA GAA T G G TAC GTCGAT Ø GTT 999909 ر ق TAC CCTTTA L TYR AGT ( AAT 9 題 T T T CA E ည ဗ Ø G AGT ⊱ ⊱⊣ ASIN ASN E E Ø A A Ø ტ ტ A A AAGA Н GIN T G A E ڻ G Ø PR0 SE ں G ⊱ C G C AT ⊱ G Ø AGC ⊱ ⊱ ILE Ø E AA Z

### FIG.21E

	<b>7</b> 9/23	35	
LYS LEU LYS SER ASN ASP ASN THR SER ASN A A G T T A A A A T C A A A T G A T A C A A G C A A C A 820 820	ASN LYS PRO LEU PRO ILE GIN PHE LEU SER  A A C A A A C C A C T T T T T T T T T T	SER PHE ASP ILE HIS ALA ASN LEU SER ALA  TCTTTTGATATACATGCCAACTTGTCAGCA 920 930 ARG SER THR GLU LEU ASN MET SER LEU ILE ARG STCAACTGAGTTAAATATGAGTTTAATT 960	ASN ILE SER ASN GLY VAL ASN PHE SER ILE A A C A T T T C T A A T G G G T T A A T T T T T C C A T A 990 970 ASN SER HIS VAL ARG GLY ASN ALA PHE A A C T C C C A T G T T C G C G G T A A T A A T G T T T T 1000 1020

PCT/CA99/00938

## 1G.21F

ILE LYS LYS ASP LEU ILE ALN ALA A T C A A A A A A G A T T T A A T T A A T G C A  1030 THR GLY SER ASN PHE ASN LEU LYS GIN THR A C T G G C T C G A A T T T T A A G C A A A C G 1080	LYS ASP LYS PHE ASP ASN SER TYR GLU LYS A A A G A T A A A T T G A C A A T A G T T A C G A A A A  1090 ASN ALA ILE PHE SER THR HIS ASN LEU THR A A C G C C A T T T T C T C A T A A C C C T A A C C A A C G C C A T T T T C T C A T A A C C T A A C C C A A C T C A T A A C C T A A C C C A T T T T	LEU GLY GLY ASN VAL THR LEU GLY GLY C T G G C G C A A T G T T A C T C T A G G T G G G 1150 GLU ASN SER SER ASN ILE LYS GLY ASN G A A A A T T C A A G T A A T T A A A G G A A A. T 1200	ILE ASN ILE ASN SER LYS ALA ASN VAL THR A T C A A C A T A G C C A A A T G T T A C A
GLU G A A	UBSTITUTE SHEET (RU	A T T	ILE A T C

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(	r	5
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LEU C T T 1260	1LE A T A 1320	GLN C A A 1380	ASP G A C 1440
HIS C A C	ASN A A C A	PHE	ALA G C C (
SER AGTO	LEU T T A A	LYS A A A T	THRACCO
THR CACG 1250	ASN A A A T T 1310	ALA 3 C T A	ASN GLY THR ACGGCACC 1430
GLY GGC	GLY 3 G A A 13	SER AGTG	ASN A A C (
ALA G C C	GLY 3 G G (	GLU 3 A A A	ASN A A C P
LEU GIN ALA HIS ALA GLY THR SER HIS LEU T T A C A G C T C A T G C C G G C A C G A G T C A C C T T 1240 1260	THR LEU THR LEU GLY  ACCCTAACCCTTGGC 1280 1280 ASN VAL SER VAL GLY GLY ASN LEU ASN ILE ASN VAL SER VAL GLY GLY ASN LEU ASN ILE AATGTATCTGTTGGGGGAAATTTAAACATA 1300	HIS ILE ASP GLY ASN CATATTGACGCAAT 1340 1340 LEU SER ILE ALA GLU SER ALA LYS PHE GIN CTTTCTATTGCAGAAGTGCTAAATTTCAA 1380	ASN LEU ASN ILE THR A A C C T A A A T A T T A C C 1400 11400 GLY THR PHE THR ASN ASN GLY THR ALA ASP G G C A C C T T T A C C A A C A A C G G C C G A C 11400 11420 11420
GLN CAA	THR LEU THR LEU CCCTAACCCT1 1280 ASN VAL SE AATGTATC	ASP ( ; A C G SER T C T	ASN ] ATA THR ACC
LEU TTA	C C T A A 1280 A A T	TATTG 1340 LEU	C C T A A 1400 G G C
: : :	THR A C C C 12 12	HIS 2 A T A 13 13	ASN 1 A C C 14
	·		
	GLU G A A A O	ASN A A A B G O	ASN A A T i
	LYS GJ A A A G <i>i</i> 1270	SER A T C A A 1330	THR AACCA 1390
	ASP LYS LYS GLU ARG GATAAAAAGAAAGA 1270	ILE GLY SER ASN ALA A T T G G C T C A A A T G C A 1330	GLY LYS THR ASN ASN GGAAAACCAATAAC 1390
	ASP GATA	ILE A T T G	GLY GGA

1640

1630

ILE   ASN   ILE   IXS   GIN   GLY   VAL   VAL   IXS   LED     1450	THR ASN ASN ACCAATAACO 1490	ASN ILE THR THR ASN ALA SER VAL ASN GIN  A A T A T C A C T C A G T C A A T C A A  1510  1520  1520  1530  1540  1550  1550  1560	J ASN ILE LYS ASP ILE A A A C A T C A A G G A T A T T 1580 1590 LYS ALA ASN ALA GLU ILE GIN A A A G C C A A C G C C G A A T C C A A A A C C C A A C G C C A A A T C C A A A C C C C A A A A A	ASN ILE SER GIN LYS GLU GLY ASN LEU THR A A T A T C T C G C A A A A A A G A A G G T A A T C T C A C G
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ILE SER SER ASP LYS ILE ASN ILE THR LYS A T T T C T G A C A A A T T A A T C A C A A A A A T T A B B A A A A A A A A A A	ARG ILE GLU ILE LYS ALA ASP THR ASP GLN GGATAGAAATTAAGGCAGATACTGATCAA 1710 1690 GLY ASN SER ASP SER GLY VAL ALA SER ASN GGGAATTCTGATTCAGGCGTAGCAAGTAAT 1740	ALA ASN LEU THR ILE LYS THR LYS GLU LEU  C T A A T C T A A A C C A A A G A G T T A  1770  THR LEU THR ASP ASN LEU ASN ILE SER GLY  ACATTAACAGACAATCTAAACAGGT  1800	PHE ASN LYS ALA GLU ILE THR ALA LYS ASP  TTAATAAAGCAGAAATTACAGCTAAAGAT  1820  1830  1810  ASN SER ASP LEU ILE ILE GLY LYS ALA SER  AACAGTGATTTAATTGGCAAGGCTAGC  1860

C A C A A A A C A....

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, A G Т A A T *P* 2050

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ASIN

SER ASP ASN SER ASN ALA LYS GIN ILE THR  A G T G A C A C G T A A T G C T A A C A A T A A C C  1870  PHE ASP LYS VAL LYS ASP SER LYS ILE SER  B
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2280

ILE A T C 2100	LYS A A A 2160	ASP G A C 2220	THR. A C T
G G T	ALA G C T	THR	LEU I T A
GLY GGA	THR ACTO	THR A C C A	THR
GLU A G A A C 2090	VAL A G T A 7 2150	THR ALA CAGCA? 2210	THR ALA THR LEU
SER T C A G 20	GLU GAA	THR ACA(	THR ACT (
ALA G C A T	VAL G T G	VAL 3 T T A	GLY 5 G A 7
VAL ASN ILE SER ALA SER GLU GLY GLY ILE GTAAATATCTCTGCATCAGAAGGAGGTATC 2080 2100	A A C C A T T A A T G C G 2120 2120 THR THR GLY SER VAL GLU VAL THR ALA LYS A C C A C A G G T A G C G T G G A A G T A A C T C T A A A A C T C T A A A C T C T	THR ILE SER GLY  TACGATTCCGGT 2180 2180 LYS THR VAL SER VAL THR ALA THR THR ASP AAGACAGTAAGTGTTACAGCAACCGAC 2220	TGGCGCAAAATT 2240 2250 ASN ALA THR GLU GLY THR ALA THR LEU THR AATGCGACAGAAGGAACTGCAACCTTAACT
ILE SATCT	ASN ALZ A A T G C 213 GLY S A G G T A 2140	SER GL C C G G 21' VAL S G T A A 2200	YS I AAA' 27 THR ACA(
ASN A A T A	ILE ALTTATHE	ILE S TTT THR ACA(	LA L CAA. ALA 3 CG I
VAL G T A A	THR I CCA 20 THR ACC	THR I CGA 80 LYS AAG	LY A GCGG O ASN ASN
: : :	THR THR ILE ASN ALA A C A A C C A T T A A T G C G 2120 THR THR GLY SER A C C A C A G G T A G C (	GLY THR ILE SER GLY GGTACGATTTCCGGT 2180 2180 LYS THR VAL SER A A G A C A G T A A G T C	GLY GLY ALA LYS ILE GGTGGCGCAAAATT 2240 2250 ASN ALA THR GLU AATGCGACAGAA(
			$\odot$
	GD 9	SER A G (	LYS A A A
	ALA G C A	ILE ATTA 0	VAL G T T ? O
	LYS A A A A A G 2110	ASP I G A T A 2170	THR VACTG
	THR THR LYS ALA GLY ACTACTAAAGCAGGC 2110	THR GLY ASP CAGGCGATA 2170	SER LEU THR VAL LYS AGTTTAACTGTTAAA 2230
	THR ACT	THR GLY ASP ILE SER ACAGGCGATATTAGC 2170	SER A G T

AAT

GGATTAP 2690

AAT

ACAATA

AGC

FIG.211N

LEU THR THR VAL LYS GLY SER ASN ILE ASP TTAACTACCGTGAAGGGTTCAAACATTGAC 2500 2520	A G T T A T T A A C G C A  2540  GIN ASP ALA THR LEU ASN GLY ASP ALA SER  C A A G A C G C C A C T A A A T G G T G A T G C A T C A  C A A G A C G C C A C T A A A T G G T G A T G C A T C A  C A A G A C G C C A C T A A A T G G T G A T G C A T C A  C A A G A C G C C A C T A A A T G G T G A T G C A T C A  2580	LYS A A A 2640	ILE
ILE ATT (	ALA G C A	ALA G C G Z	ILE
ASN AACA	ASP GATG	THRACT	ASN
SER TTCAA 2510	ASN GLY AATGGTG 2570	ASN VAL THR ACGTAACTG 2630	nen Ten
GLY G G T	ASN A A T	ASN A A C	GLY
LYS A A G	LEU CIA	. GLY G G T ,	ASN
THR THR VAL LYS GLY CTACCGTGAAGGGTT 2500.	N GLU GLY THR LEU VAL ILE ASN ALA CGAAGGCACCTTAGTTATTAACGCA 2530 2550 GLN ASP ALA THR LEU CAAGACGCCACACTAA	P ARG THR GLU VAL ASN ALA VAL ASN  CCGTACAGACTCAAC 2590  ALA SER GLY SER GLY ASN VAL THR ALA LYS GCAAGCGCTCTGGTAACGTAACTGCGAAA	A A G C A G T G T G A A T A T C A C T G G A G A T  2650 2650 LEU SER THR ILE
THR ACC	ASN A A C G ALA ALA C C C C	LA VAL ASI CAGTCAA 26. SER GLY S	SLY Z G A G
THR AAC1	ILE ATTA ASP ASP	ALA ; C A G SER A G C	I ILE THR GI TATCACTG ( 2660 LEU SER
T. T. A. A.	VAL A G T T A 2540 GIN C A A	G A A T G C 2600 ALA G C A A	ILE LA T C A 2660 LEU
: : :	LEU P T A ( 25	VAL 3. T. G. P. 26 26 27 27	ASN A T A 26
	THR A C C 7	GLU 3 A A C	VAL 3 T G A
	GLY G G C Z	ARG THR GTACAG 2590	SER G T G
	ACGAAGGCACCTTAC 2530 2530	ARG 7. 2590	SER A A G C A 2650
	J C	О Д	R A A

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### FIG.21N

SER LYS ASN GLY LYS ASN THR VAL VAL LEU  C G A A A A A G G T A C C G T A G T G T T A  2720  2730  LYS GLY ALA GLU ILE ASP VAL LYS  A A G G T G C T G A A T T G A T G T G A A A  A A A G G T G C T G A A T T G A T G T G A A A  2750  IN PRO GLY VAL ALA SER ALA ASN GLU VAL  A A C C A G G T G T A G C A A G T G C G A A T G A G G T T  2770  2780  2780  2780  2790  ILE GLU ALA LYS ARG ALA LEU GLU GLU  2790	GTGCCTTC 2810 GLY VAL SER GTGTAAGTG 2870
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SER A G T

... GCGTGTTTCTCA

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GIN VAL THE ILE SER GLU GLY PHE THR ARG PROCEASING THE GLOUNTE THR ARG PROCESSOR S930 S930 S930 S930 S930 S930 S930 S930
  VAL THR ILE S GTGACAATTT
VAL G T G
VAL G T G
VAL G T G
GIN

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G C T G A C G A T G G A C A G... 3020 ... CAGTAG ASP ALA GTT VAL ACCAAT ASIN

180

LCDC2 hmw1A sequence

<del>[ |</del> PRO AC G G H C Ø 国 G TRP  $\mathfrak{O}$ GEU LYS A A

ALA GLY ...VAL

AC ASP G G Z,  $\mathcal{O}$ Ŋ G A G K A C ... T A

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ARG

GLY

VAL

GLU GLY  $C \subset T$ THR CTGCTTTC K  $\circ$ Ø G

AGA ARG GGAA <u>ე</u> ACA CCGGA

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> ACA ATA CCAACA PR AGA ARG  $\mathcal{O}$ ASN Ø Ø, K Ø ں

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### FIG.22E

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THR ACC'

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ASN SER GLY VAL GIN ILE ASP CAACAGCGCGTTCAGATTGAT 280	ILE THR SER ALA THR GLY GLY  FATTACTTCCGCTACTGGCGGAA  310 SER LEU THR VAL TYR SER SER GLY TRP VAL ASP GCTTAACCGTTTACTCTAGTGGCTGGGTTGAT  350  360	VAL HIS LYS ASN ILE THR LEU ASN SER G T T C A T A A A A C A T T A C A C T T A A T T C A G 370
GLU ASN SER HIS J GAGAACTCCCACC 250	GLY ASN ILE THR SGCAATATTACTT 310	VAL HIS LYS ASN ILE STTCATAAAACATTA 370
	LEU ILE LEU TRP SER  TAATCCTCTGGAGCG  260 GLU ARG ASP GLY ASN SER GLY VAL GIN ILE ASP AAAGAGATGCAACAGCGCTTCAGATTGAT  280  300	ASN SER GLY VAL GIN ILE ASP CAACAGCGCGTTCAGATTGAT 300 300 TYR SER SER GLY TRP VAL ASP TTACTCTAGTGGCTGGGTTGAT 360

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	92/23	35	
GLY TYR LEU ASN ILE THR THR LYS SER GLY ASPGGTACTTAACATTACGACTAAAGTGGAGAT390 400	VAL ALA PHE GLU GIN GLY ASN ASP LEU G T C G C C T T C G A A C A A G G A A T G A C C T A A 430THR ILE THR GLY GIN GLY THR ILE THR ALA SER C C A T T A C A G G T C A A G G A A C T A T T A C C G C A A G G 450 480	LYS LYS GLY PHE ARG PHE ASP ASN VAL  A A A A A A G G T T T T A G A T T T G A T A T	LYS TYR SER GIN THR ASN ASN LYS  A A T A C A G C C A A A C A A T A A T A A G  550 ASP SER ASN PHE GLU ASN HIS PHE ARG GLY THR  A T A G C A A T T T C G A A A C C A T T T T A G A G G A A C T  570  580  500

VAL GTA 620

E SER GLY
TTCAGGG7

1E

LEU ASN TTAAATA

ARG HIS SER GLY ARG SER HIS TRP ASN  AGACACCACGAAGCAAGCAAGCAAGCAAGCAAGCAAGC	LEU ASN ILE THR ILE ASP ASN SER GLY  CTCAACATCACTATTGATAACAGTGGCA  740 SER ARG PRO SER PRO GLY ALA GLY PRO LEU TYR GCCGTCCATCCCTGGTGCCCTCTATAT  780	ARG ARG SER GLY LEU ASN GLY ILE SER A G A C G T T C G G C A T A T C G T 790 800

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PHE ASN ASN ASP THR VAL PHE ASN VAL ALA SERTTAACAATGACACTGTTTTAATGCGTCA810 820 840	GLY SER ALA VAL ASN PHE SER ILE LYS  GGTTCGGCAGTTAACTTTAGCATCAAGC  860 PRO PRO ILE VAL SER ASN VAL HIS ASP GLY ASN CACCAATAGTAAGCAATGTACACGACGGGAAT  890  900	HIS THR LEU PHE ASN GLY ASN VAL SER  CACACATTATTCAATGGAATGTTTCAG  1  920 VAL LEU GLY GLY GLY ASP VAL ASN PHE HIS PHE TTTTAGGGGGGGGATGTCAACTTTCATTTT  950	ASN ALA SER SER ASN HIS TRP THR  A A C G C C T C C A C C A C C A C T G G A C T C  970 HIS GLY VAL VAL ILE LYS SER GLN ASN PHE ASN  A T G G C G T G G T T A T A A G T C T C A A A A C T T T A A T  A T G G C G T G G T T A T A A A G T C T C A A A A C T T T A A T  1020

ALA SER GLU GLY SER SER LEU ARG PHE  G C C T C A G G T C A G C T T A A G A T T C A  1030 LYS SER GLU GLY SER THR ARG THR ALA PHE THR  A A A G C G A A G G T T C A A C C G C T T T T A C A  1080	ILE GLU SER ASP LEU THR LEU ASN ALA A T A G A A G T G A T T T A A C T T T A A T G C C A 1090THR GLY GLY ASN ILE SER LEU ASN GLN VAL ALAC T G G G G C A A T A T A T C A T T G A A C C A A G T T G C A1110 1140	GLY ILE ASP GLY ASN LEU GIN LYS SER  GGTATTGATGGTAATCTCCAAAAAGCC  1160 LEU VAL ALA ASN LYS ASN ILE THR PHE GLU GLY TTGTAGCCAATAAAACATAGGGG  1200  1200	GLY ASN ILE THR LEU ALA ALA ASP LYS GGCAATATCACCCTTGCAGCCGATAAA 1210 1220
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VAL G T T 1260		ASN A A T 1380	SER C A G C 1440
LYS PRO ILE GLU ILE LYS GLY ASN ILE THR VAL A A C C A A T A G A A A T C A A G G T A A T A T T A C T G T T1230 1240 1260	CACCCTTCGTA  1280  SER ALA ASN TYR GLY ASN ASP LYS SER ALA LEU GCGCGAATTATGGTAATGACAAATCAGCTTTA GCGCGAATTATGGTAATGACAAATCAGCTTTA1290	CACTAATAAAG  1340GLY ASN LEU THR VAL THR GLY SER ALA ILE ASNGCAATCTCACGGTTACGGCTCGCTATCAATGCAATCTTACTGTTACTGGCTTTATTATTATTATTATTATTATTATTATTATTATTATT	VAL GLU GLY  CGTTGAAGGTA  1400   SER ALA LYS PHE LEU ALA ASN PRO ASN TYR SER  GTGCTAAGTTTTAGCTAATCCAAATTACAGC  GTGCTAAGTTTTAGCTAATCCAAATTACAGC
ASN ILE A A T A T T A !50	SER T C A	ALA G C T	ASN A A T'
ASN A A T 1250	ASP LYS SER 3 A C A A A T C A G 1310	/ SER CTCC 1370	PRO F C C A A 1430
GLY G G T	ASP G A C	GLY GGC	ASN A A T C
GLU ILE LYS GLY BAAATCAAAGGT <i>P</i> 1240	ASN AATG	THR ACCG	ALA G C T
AAATC 1240	ARG C G T A ASN TYR GLY A A T T A T G G T P	VAL GTTA	LEU TTAC
GLU AGAA 12	ARG CGTA ASN TYR A A T T A T 13	ASN LYS A A T A A A G ASN LEU THR VASN LEU THR VASO C G	 A PHE I T T T T 1420
ILE	ARG F C G T ASN ASN	LYS LEU CTC	GLY G G T LYS A A G
PRO A C C A A )	THR LEU CCCTT(80 SER ALA GCGCG7 1290	THR ASN LYS CTAATAAA 40 3LY ASN LEU GCAATCTC	VAL GLU GLY TTGAAGGGOO 00 SER ALA LYS GTGCTAAG
LYS A A C	C A C C C T T 1280 SER ALA G C G C G	CACTAATAAAG 1340 CLACTAATAAAG 1340 CLY ASN LEU THR GCAATCTCAC(	ILE GLU LYS ASN LEU THR VAL GLU GLY A T A G A A A A A T C T T A C C G T T G A A G G T A 1390SER ALA LYS PHEG T G C T A A G T T T
			THR ACC
	ASN A A	ASN A A T G	LEU CTTA
	17 ALA 3 A G C C 1270	KG GLY S A G G A A 1330	ASN A A T
	GLY GGA 12	ARG A G A G 1330	LYS 7 A A A A 1390
	LYS GLU GLY ALA ASN VALA A A A A B A B B B B C C A A T G T 1270	SER ILE ARG GLY ASN VAL A G T A T A A G A G G A A A T G T 1330	ILE GLU LYS ASN TAGAAAAAATC 1390
	LYS A A A	SER A G T	ILE A T A

# FIG.22H

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TTTAACGTATCCGGCCTATTTGACAACC  1450GIN GLY LYS SER ASN ILE SER ILE ALA LYS GLYGAGGCAAGTCAACATTCCATTGCCAAAGGAAAGGCAAGTCAAACATTCCATTGCCAAAGGA 1500	GLY ALA HIS PHE LYS ASP ILE ASN ASN GGGGCTCACTTAAAGACAL 1510THR LYS SER LEU ASN ILE THR THR ASN SER ASPCTAAGAGTTTAAACATTACTACCAACTCCGACCTAAGAGTTTAAACATTACTACCAACTCCGAC1530 1560	SER ALA TYR ARG THR ILE ILE GLU GLY  TCCGCTTACCGCACTATTATAGAAGGCA  1570 ASN ILE THR ASN SER ASN GLY ASP LEU ASN ILE ASN ILE THR ASN SER ASN GLY ASP LEU ASN ILE ATATAACCAACAGTAACGGGGATTTAAATATC 1590  1600  1600	THR ASP ASN ASN ALA GLU ILE ACTGATAATAAATAACGCTGAAATCC 1630 1640
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GIN ILE GLY GLY ASN ILE SER GIN LYS GLU GLY A A A T T G G C G C A T A T C T C G C A A A A G A A G G T1650 1660 1670 1680	ASN LEU THR ILE SER ASP LYS ILE A A T C T C A C G A T T T C C G A T A A A T T A 1690 1700	ATATCACTAACCAGATAACAATCAAGAAGGGT1710 1720 1730 1730	VAL ASN LYS GLU ASP SER SER SER G T T A A T A A G A G G A T T C A A G C A 1750 1760	THR ALA ASN ASN ALA ASN LEU THR ILE LYS THRCGGCAAACAATGCTAATCTAACCATTAAAACC 1780 1790

TTGCAA 1810 GIN E GAA GLU AAA

TTA [EG]

A C G G G A G A C C T A A... 1820 . ASN

LEU

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' A A A G C A G 1850 TCAGGCTTCGAT ASP GLY

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GTA 1980 0 6 6 7 VAL <u>-</u>-AAT ASIN A A Ø K CACI ALA AAT ည ဗ ASIN AACAAT GACAGT ASIN GAAAGC SE SER ASN ASP GLU AAC  $G \subset T$  $C \subset T$ ASN ALA ALA GATAAT ATCTCT AATGAC ASIN SER ASP 1900 AACCAGGTTAAAG... ASIN AGT ... ATTCGAAA ACCTCT AAT GCA LYS ASIN C E-... GTAAT ASIN AAT .. A T G G C SER 開 GLY ASIN Ø GATTTA GTAGAA ...1890 · · · GLY GLN ...ASP ACTATT ...1950 . ASIN ...2010 ILE 1940 ASIN VAL 盟  $C \subset C$ TLL AAA TTA LYS 国 GAGGGT AACC ACAGT ACCAGC 開 SER SEC WAL ASN E G K AAA A A Z 2099 园 ى Ø CA⊱ K GA

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SER T C T 2100	ILE A T T 2160	VAL G T T 2220	ASN A A C 2280
THRACTI	THR	LYS A A A	SER A G C
ILE A T T A	GLY THR 5 C A C A A 50	G G T A	VAL G T A A
ASN 2090	GLY 5 G G C 2150	LYS F A A A G 2210	ALA 1 G C T G 2270
ASN ASN ASN AACAACAATA 2090	ALA G C G G	ILE A T T A 22	LEU CTTG 22
LYS ASN ILE THR VAL ASN ASN ASN ILE THR SERAAAATATACAGTAAACAACAATATTACTTCT 2000 2000 2100	THR ALA SER  ACTGCGTCAG GLU ASN VAL THR LYS ALA GLY THR THR ILE .AAAATGTTACCACCAAAGCGGCACAACCATT .2130 .2130	VAL GLU VAL G T A G A A G T A A 180 THR ALA LYS THR GLY ASP ILE LYS GLY LYS VAL . C A G C C A A A C A G G T G A T A T T A A A G G T G A T A T	VAL THR LEU 3 TAACACTTA 240 THR ALA THR GLY GLU ALA LEU ALA VAL SER ASN CTGCAACCGGAGAGCTCTTGCTGTAAGCAAC 2250 2250
LYS ASN ILE THR VAL AAATATAACAGTAA 20070 2080	  HR THR CCACCA 2140	  R GLY 2200	GLU GAAG SO
THR A C A 20	THR ALA SER ACTGCGTCAG 120 GLU AŞN VAL THR .AAAATGTTACCA.	GLU VAL 3 A A G T A A ALA LYS THR 5 C C A A A A C A (220)	 A GLY ( G G A G
ILE ATA	THR ALA SER ACTGCGTCAG 120 GLU ASN VAL THR . A A A T G T T A C	VAL GLU VAL G T A G A A G T A A 180 THR ALA LYS THR . C A G C C A A A A C C	VAL THR LEU G T A A C A C T T A 240 .THR ALA THR GLY . C T G C A A C C G G 22550
ASN A T	THR ALA A C T G C G 120 GLU ASN A A A A T 2130	VAL GLU VAL GTAGAAGT 180 THR ALA LYS . CAGCCAAA	VAL THR GTAACAC 240 THR ALA ' CTGCAA.
LYS A A	$\sim$ 1	$\sim$ 1	$\mathcal{O}_{\mathcal{C}_{3}}$
	ILE ATC	SER AGC	SER TCT
	ASN A A T A	THR GLY ACAGGT? O	SER GLY CCGGCT
	VAL G T A A O	TTR ACA 0	SER T C C O
	LYS THR VAAACAG	THR 7 ACCA 2170	SER THR SUCCACTT
	HIS LYS THR VAL ASN ILE CACAAAACAGTAAATATC 2110	ASN ALA THR THR GLY SER A A T G C A A C C A C A G G T A G C 2170	SER T C C
	HIS CACA	ASN A A T	GLU SER THR SER GLY SER GAATCCACTTCCGGCTCT 2230

### FIG.22L

GLY GGC7

ILE SER ATTTCA(

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GLY 3 G C 2340	GLY 3 G T 2400	GLY 3 G C 2460	
ALA GLY 3 C A G G 0 234	SER AGCG	SER CCG	
THR THR GLN ACAACTCAAG 2330	ILE ATT?	THR LYS SER	
THR AACT ( 2330	ASP C G A T A 2390	THR FACTA 2450	
THR ACA 2	GLY COG	THR ACTA 24	
2300 AIA ASN LYS GLY LYS LEU THR THR GLN ALA GLY CAAATAAGGGTAAATTAACAACTCAAGCAGGC 2310 2320 2340	SER PCA	VAL LYS VAL  A G T A A A G T T A  2420 SER ALA ILE GLY ASP LEU THR THR LYS SER GLY GTGCGATCGTGATTGACTAAATCCGGC 2430  2440	
LYS A A A A 0	GIN C A A 1 0	ASP 3 A T T	
GLY I G G T A 2320	GLY VAL  GGTGTAA   ALA SER SER (  GCTCAAGCC  2380	LYS VAL A A A G T T A ALA ILE GLY A C G A T C G G T G 2440	: : : : : :
LYS A A G	VAL GTA SER TCA	VAL GTT ILE ATC	GLU GAG
ASN A A T	ASN GLY ACGGT 60 THR ALA CTGCC 2370	VAL LYS VAL TAAAAGT 20 SER ALA ILE GTGCGATC	THR GLY GLU CAGGTGA( 80
2300 ALA ASN LYS GLY C A A A T A A G G G T A	ASN T A A C ( 2360THR C T G	VAL A G T A A 2420SER G T G	THR AACA 2480
	ILE ATT ,	THR ACA	LYS A A A
	ALA G C G A	ASN AACA	ALA G C A
2290	ML SER LTAGCG 2350	SER GLY CCGGTA 2410	LYS A A G 70
22	THR VAL 1 C G G T T A 2350	SER 1 C C 24	ILE I ATCA 2470
	SER THR VAL SER ALA ILE ASN GLY VAL TCTACGGTTAGCGCGATTAACGGTGTAA 2350 2350 2350THR ALA SER SERCTGCCTCAAG	THR ILE SER GLY ASN THR VAL LYS VAL ACGATTCCGGTAACACAGTAAAGTTA 2410 2420SER ALA ILE GLYGTGCGATCGG'	SER GLU ILE LYS ALA LYS THR GLY GLU TCGGAAATCAAGGCAAAAACAGGTGAGG 2470 2480
	SER TCTA	THR A C G A	SER T C G

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GLY G G T 2520	N ALA VAL ASN TGCAGTAAATG 2540VAL THR ALA ASN THR GLY ASP LEU THR VAL GLUTTACAGCAAATACTGGCGATTTAACTGTTGAA2550 2570 2580	LYS A A A 2640	ALA G C T 2700
ILE A T T	VAL G T T	GLY 3 G C 1	SER ICAG
THR ACAA	THR A C T	SER I C G G	LEU
GLY A G G T 2510	ASP LEU THR 3 A T T T A A C T ( 2570	THR AACA: 2630	ASN LEU AAACCTTT 2690
ALA THR GLY CGACAGGTA 2510	ASP 3 A T C	ALA THR 3 C A A C A T 2630	VAL TAA
ALA 3 C G <i>I</i>	GLY 3 G C (	THR	ASN GIN VAL NACCAGGTA?
SER AGTO	THR ACT(	LEU TAP	ASN . A C C
ALA ASN VAL THR SER ALA THR GLY THR ILE GLYCTAACGTGACAAGTGCGACAGGTACAATTGGT2490 2520	ASN A A T G  AIA ASN THR GLY C A A A T A C T G G C (2)	P ALA THR GLY TGCGACAGGAG 2600GLY ALA ALA THR LEU THR ALA THR SER GLY LYSGAGCCGCGACCTAACTGCAACATCGGGCAAA 2620 2630	r 2
VAL G T G Z	ASN A A T ( ALA 3 C A A	P ALA THR GLY T G C G A C A G G A G 2600GLY ALA ALA THRGAGCCGCGAC	T T C A A G C A T T A 2660 THR SER ALA ASN C T T C A G C T A A C
ASN A A C	T G C A G T A A A S 2540 VAL THR ALAT T A C A G C P	ILE ASP ALA THR GLY TTGATGCGACAGG 2600GLY ALA ALAGAGCGCGGAGCGCC	SER ILE AGCAT' SER ALA FCAGCT
ALA C T	T G C A 2540VAL T T T2550	P ALA T G C G 7 2600 GLY G A G	ALA SER SER  C T A G T T C A A  2660 THR  C T T  C T T
: : :	ASN A A T 2 2	ASP G A T 2	SER A G T 2 2
	GLY G G T	ILE A T T	ALA G C T
	ILE SER GLY ASN TTTCTGGTAA7 2530	ALA ALA LYS ; C C G C A A A A A 2590	THR THR LYS
	ILE & ATTT 2530	ALA I G C A A 2590	THR I A C T A 2650
	GGTACGATTCTGGTAATGCAGTAAATG GGTACGATTTCTGGTAATGCAGTAAATG 2540VAL THR ALA ASN 2550VAL THR ALA ASN 2550	ASP ALA ALA LYS ILE AS GATGCCGCAAAATTGA 2590	LEU THR THR LYS ALA SET TTAACCACTAAGGCTAG 2650
	G G T	ASP G A T G	LEU '

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TCCGGCAGCGT

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AACAGCGGCACCTTGGTT TGAAT GTAGTG ASIN EE E B VAL ں ACA Ø THE ... CATCAGGTAACCATA AATGTA WAL 段 HIS ASN ASIN AAGGGTTCAAGCA... : : C L ... TTAACGCA ... A T G C T  $\vdash$ CTAAATGGT ASN AA GGGGGA ...2790 ...ILE GLY ...ASIN GLY ASIN ...ALA GLY 园 Ľ GAG CTACCGTG WAL Ø GGTAGC ⊢ 段 当 ACGC GLY Ø G GAT TA AAA ASP EEG AAG E ď, LYS

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GLY	LEU	GLU	GLU
G G G	C T G	G A A	3 A A
2940	3000	3060	3120
THR	VAL	ASP	ARG
ACTO	G T A (	3 A T (	A G A (
ILE	THR	VAL	GLU
A T C	A C C (	3 T A (	3 A A A
VAL ASN ILE	ILE ASN THR	ALA SER VAL	ASP GLU S A T G A A C 3110
FTGAACATCA	TAAACACCG	3 C A A G C G T A C	
2930	2990	3050	
VAL	ILE	ALA	ASP
G T G	A T A 2	3 C A 7	3 A T C
ARG	GLY	ILE	SER
A G A G	G G T	A T A G	FCTG
SER SER CAAGCA 2920	ASN A A C (	GLY G G T P	LEU FTA 7
ALA THR THR SER SER ARG VAL ASN ILE THR GLY CGACAACCTCAAGCAGAGTGAACATCACTGGG2910 2920 2930	GLY LEU ASN TGGATTAAATA 2960ILE ILE SER LYS ASN GLY ILE ASN THR VAL LEUTCATTTCAAAAACGGTATAAACACGTACTG	ASP VAL LYS  TGATGTGAAAT 3020 TYR ILE GIN PRO GLY ILE ALA SER VAL ASP GLUACATTCAACCGGTATGAA 3050 3040 3050	ILE LEU GLU A T C C T T G A G A 1080 LYS VAL LYS ASP LEU SER ASP GLU GLU ARG GLU . A G G T A A A G A T T T A T C T G A T G A A G A G A A G A A A G A A G A A A G A G A A G A G A A G A A G A G A A G A G A A G A G A A G A G A A G A G A A G A G A A G A A G A A G A G A G A G A G A G A A G A
THR ACCT	GLY LEU ASN GGATTAAATA 2960 ILE ILE SER LYS .TCATTTCAAA	ASP VAL LYS G A T G T G A A A T 3020 TYR ILE GIN PRO A C A T T C A A C C C 3.3030	LEU GLU C T T G A G A VAL LYS ASP G T A A A A G A 3
THR ACAA	GLY LEU GGATTA? 2960 .ILE ILE .TCATT	VAL GTGP ILE	ILE LEU GLU CATCCTTGAC 3080LYS VAL LYSAGGTAAAA
. C G A	GLY G G A 2960 .ILE .T C	ASP F G A T G 3020 TYR A C A	ILE LEU 3 A T C C T T 3080LYS VAL A G G T A
: : :	ASN A T	ILE ATT 3	
	ILE	LYS	ALA LYS
	A T A	A A A A	S C G A A A C
	THR	VAL	ALA
	ACA 7	G T T 2	G C G
	50	10	70
	ILE A T C A 2950	LYS GLY \\ A A G G C G 3010	GLU A GAAG 3070
	ASP LEU ILE THR ILE ASN GATTAAT 2950		VAL ILE GLU ALA LYS ARG GTAATTGAAGCGAAACGC3070
	ASP	LEU	VAL
	GATT	TTA?	G T A

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### FIG.22P

AIA LYS LEU GLY VAL SER ALA  3 C T A A A C T T G G C G T A A G C G C T G  3130 VAL ARG PHE ALA TACGTTTTGC  3.3150  A C A C A A A T G A G T T T A C A C C A  3200  3200 ARG PRO SER SER GACCATCAAG ARG PRO GT T T A C A C C A  3200  3200 ARG PRO SER SER ARG PRO SER SER GACCATCAAG 3210
ALA LEU GCGTTAGGCGTTAGGILE ASN CLYS VAL (

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...AIA THR ILE CYS THR ASN ILE ALA ...CAACAATATGCACCAATATTGCT( ...3270 3280 3290

> ARG \*\*\* CGGTA(

## FIG.23A

ICDC2 hmw2A sequence

	LYS GLU TRP LEU LEU ASP PRO ASP ASP  A A A G A G T G G T T A G A C C C G G A T G A T G  10 VAL SER ILE ASP ALA PRO SER ALA GLU ARG THR TATCCATTGACGCACCTTCGGCTGAACGCACTTATCCATTGACGCACCTTCGGCTGAACGCACT 30  40  60	ASP THR GLY GLU ASP VAL GLU TYR THR GACACTGGCAATACACCG   80 GLY THR GLY ALA ASP ILE ASN HIS GLN LYS GLN GAACAGGGGTGATATTAACCATCAAAACAA  120	ASN SER GLU THR LYS SER THR LEU THR  A A C A G C G A A C C A A G T C A A C A T T A A C A A  130 ASN THR THR LEU GLU GLY MET LEU LYS ARG GLY  A C A C A A C T C T T G A G G G G G  180  110
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ALA G C G 480	LEU T T A 540	LEU CTT 600
ILE	SER T C T	ARG A G A
ILE A T T	VAL G T G	HIS C A T
GLN C A A 470	ASN A A T 530	SER TCT
ALA G C T	ASN A A C	LEU PTAT
SER A G T	LEU	LEU SER ILE  TAAGTATTA 60 ILE SER THR ALA SER ASN LEU SER HIS ARG LEU TTTCAACAGCAAGCAATTTATCTCATAGACTT 570 570 570
ALA G C A	ARG A G A O	SER AGC
 G SER T C A	 A PHE T T T	 A AIA G C A A 580
LYS A A A SER A G C	GLU GAA THR ACC	ILE ATT? THR ACAG
ASN A A T ARG C G T	GLY GGA LYS AAA	LEU SER ILE CTAAGTATT 560 .ILE SER THR .TTCAACA
GLY G G C 440 .GLY . G A		7 \ 10 \ \
ASN A A C		GLY G G T C
GLY G G A	THR A C T	ASN A A T G
GLY G G T O	ILE A T A O	THR GLY 1 C G G G T 7 550
GLU GAG 43	THR A C T 49	THR (A C G G 550
PHE T T C	GLY G G T	ASN GLY THR GLY ASN GLY AATGGGACGGGTAATGGT 550
ALA G C T	GIN C A G	ASN A A T
	GLY ASN LYS GGCAATAAAG 440GLY ARG SER SER ALA GIN ILE ILE ALAGACGTAGCTCAGCAAGTGCTCAAATTATCGCGGACGTAGCTCAGCAAGTGCTCAAATTATCGCG450	ALA SER ALA GIN ILE ILE ALA A G C C A A G T G C T C A A A T T A T C G C G 460 460 470 480 480 ARG LEU ASN ASN VAL SER LEU T A G A C T C A A C A A T G T G T C T T T A 520 530 540

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# FIG.23D

ASP GLY GLU ILLE ASN VAL SER GLY ASN G A C G G T G A A T T T A T G T A T C T G G A A A T G 610VAL THR ILLE ASN GLN THR THR GLN GLN ASN ILLETAACAATTAATCAAACCACGCAGCAAAACATT 660 660	GLU TYR TRP LYS ALA SER SER ASP SER GAATACTGGAAGGCTAGCAATTCTT 670TYR TRP ASN VAL THR SER PHE ASN LEU ARG GLUATTGGAATGTCACTTTTTAATTGAGAGAA 720	ASP SER LYS PHE THR PHE ILE LYS TYR GATTCAAAGTTTACCTTTATCAAATACG 740VAL ASN SER ALA ARG ASN GLY ASP VAL ARG GLYTTAACTCTGCCAGAAATGGTGATGTAAGAGGA 780TTAACTCTTGCCAGAAATGGTGATGTAAGAGAGAA	ARG SER PHE ALA GLY VAL ILE PHE ASN A G A A G T T T G C A G G T G T A T T T A A T G 790 800
AS T A A	AI 3 G C	F A C	A G G
ILE A T C	LYS A A (	PHE T T T S	ALA G C 7 0
GLU GAA 6.	TRP T G G	LYS A A G	PHE I T T 75
GLY	TYR .	SER	SER G T
ASP GLY GLU GACGGTGAAA	GLU TYR TRP GAATACTGG1 67(	ASP SER LYS GATTCAAAGT	ARG SER PHE AGAAGTTTTO 790

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ALA LYS GLY LEU THR THR SER PHE ASN VAL LYS CTAAAGGTCTCACTACAAGCTTTAACGTCAAG 810 820 830	AL ASP PHE LYS LEU  TTGATTTTAAATTAA  860 LYS PRO ASN SER GLY TYR ASN SER GLN LYS ARG GLY TYR ASN SER GL	HE GIN SER ASN II.E  TCCAATCCAACATCT 920SER VAL SER GLY GLY ARG VAL ASN II.E ASNCGGTCTCAGGAGGAAGGGTAAACATTAACCGGTCTCAGGAGGAAGGGTAAACATTAAC930 940	THR GLY GLY GLY  FTACAGGCGAGGAG  980 VAL GLU ILE ARG SER SER ILE ASN VAL SER TGAGATAAGATCGAGTTCAATTAATGTTTCT  1020
ALA LY C T A A 810	LIS GLY SER THR VAL ASP PHE LY A A G G C T C G A C A G T T G A T T T T A A 850LYS PR A G C C 870	<b>.</b>	96

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ASP GLY G A T G G C

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THR 1 C C 1080		GLY 3 G T 1200	
THR 'AC(	GLY G G 7 114(	GL G G 12	
ILE ATTA	ASP 3 A T (	GIN	
LU A A A	NS T A	日 日 日	
T G	AAA	I A T	
PHE CTTT 1070	GIN 5 C A A 1130	THR 1 A C T 1190	
ARG ASN ALA PHE GLU AGGAATGCCTTTGAAA 1070	ILE GIN GIN ASN TACAGCAAAATO	VAL T A 1	
NA DE 1	E (	S O	
A A B	II	AS PAA	
ARG A G (	ILE A T ?	TYR TA1	
ALA  C T C  ARG ASP A C C C A C A 1060	 T SER ILE ICTATTA	A LYS TA A A T 1180	: : :
ARG	ASN A A T LEU	ALA 3 C C . SER	ASN A A T
ACAC ACAC ALA 3 C T C	ALA SER ASN CAAGCAA1 00 SER ASN LEU CAAACCTA	ALA ASN ALA CAAATGCC 60 ILE ASN SER TTAACTCA	GLY GIN ASN GGCAAAAT
GATGGCTCAACCCTCTATGACAGCTC  GATGGCTCAACCCTCTTATGACAGCTC  1030 GIN ALA ARG ASP ARG ASN ALA PHE GLU ILE THR AGGCTCGCGACAGGAATGCCTTTGAAATTACC  1080	LYS ASP LEU VAL II.E ASN ALA SER ASN A A A G A T T T A G T T A T A A A C G C A A G C A A T T  1090SER ASN LEU SER ILE ILE GIN GIN ASN ASP GLYC A A A C C T A T C T A T T A T A C A G C A A A T G A T G G A1110	PHE ASP ASN ASN GIN LYS ALA ASN ALA  TTTGATAATAATCAAAAGGCAAATGCCA  1150 ILE ASN SER LYS TYR ASN VAL THR ILE GIN GLY TTAACTCAAAATATATAACGTAACTATTCAAGGT 1170	GLY ASN VAL THR LEU GLY GLY GIN ASN GGTAATGTTACCCTTGGCGGGCAAATT 1210 1220
	ASN A A C. (	LYS A A G ( 1	GLY 3 G C (
ASF GLICAACCCTCTCTCTTTT 1030	ILE A T A A	ASP ASN ASN GLN ATAATAATCAAA 1150	ASN VAL THR LEU GLY A A T G T T A C C C T T G G (
A C C C	VAL 3 T T A	ASN A A T (	]]] ] C C (
C A A 1030	LYS ASP LEU VAAGATTTAG	ASN A A T A 1150	AL 1 TTA 1210
CT	)P T T T	. Т. А.	N E
1 G C	A.G. A.	AS F G A	AS A A
G A C	LYS A A i	PHE TTTG	GLY GGTA

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ILE A T T 1260	LEU C T A 1320	ILE A T T 1380	LEU C T A 1440
ASN A A T A	LYS A A G	ASN A A C 7	ASN A A C (
VAL 3 T T A	LYS A A A A	ALA 3 C A 1	ASP 3 A C A
SER 3 A G T G 1250	; ASN A A A T A 1310	A SER A A A G T G 1370	ASN A A A T G 1430
GLY G G G J	ARG A G A A 13	ALA G C A P 13	THR ACAA 14
ILE THR	ASP G A T A	VAL GLY STTGGC(	ALA GLU ; C A G A A A
SER SER THR ILE THR GLY SER VAL ASN ILECAAGCAGTACAATCACAGGGAGTGTTAATATT1230 1240 1250	THR LEU GLN A C T T T G C A A G 1280 ALA HIS ASN GLY ASN ASP ARG ASN LYS LEU . C C C A C A A T G A T A G A A A A A A A G C T A 1320 .1290	VAL GLU GLY G T T G A A G G A G 1340 GLU LEU ARG LEU VAL GLY ALA SER ALA ASN ILE .GLU LEU ARG LEU VAL GLY ALA SER ALA ASN ILE .A A T T A A G G C T A G T T G G C G C A A G T G C A A G T 1350 1350	
THR 1 ACAA 1240	GLN C A A G  ASN GLY A A A T G G C A 1300	GLY 3 G A G ARG LEU V 1360	 G LYS A A A G 1420
SER A G T A	THR LEU GIN A C T T T G C A A G 1280 ALA HIS ASN GLY C C C C C A C A T G G (1290)	VAL GLU GLY G T T G A A G G A G 1340 GLU LEU ARG LEU . A A T T A A G G C T 1350	GLY GGT PHE TTC
SER A G C A	THR LEU A C T T T G ( 280 .ALA HIS . C C C A C P .1290	VAL GLU G T T G A A ( 1340 .GLU LEU . A A T T A A .1350	LYS SER GLY A A G A G C G G T 400 ALA LYS PHE C T A A A T T C .1410
. C A A . 1230	THR A C T 1280 ALA C C	VAL G T T 1340 GLU	LYS A A G 7 1400 .ALA C T A
: : :		SER TCT 1	
	ALA ASN CAAATO	VAL SER GTATC	ASN LEU SER AATCTTAGT( 1390
	ALA G C A	ASN A A T G	LEU CTT
	ALA ASN A CTAATG 1270	PHE GLY A TCGGTA 1330	ASN I A A T C 1390
	GLY ALA ASN ALA ASN VALGGCCCTAATGCAAATGTT 1270	THR PHE GLY ASN VAL SER ACCTTCGGTAATGTATCT 1330	ASN ASN LEU SER VALA A CAACAATCTTAGTGTT 1390
	G G C G	THR ACCT	ASN A A C A

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ALA	G C G 1500	ASN A A C	THR	1620
LYS GLY	GCACCTCCATAATTGATGTAAAAAAGGGGCCG1470 1480 1500	THR ASN ASP  TACCAATGATG  1520  GLY ASN LEU ASN ILE THR THR ASN ALA LYS ASN 1520GTAATTTAAATATCACTACTAATGCTAAAAAC	ASN GLY ASN CAACGGAAATA 1580ILE THR ASN ASN LYS GLY ALA LEU ASN ILE THR	
LYS	AAA	ALA G C T A	ASN A T A	, 
LYS	1490	ASN A A A T G	ALA LEU	1610
VAL	GTA	THR THR	ALA	· ` ` '
ASP	GAT	THR	LYS GLY	1 1
ILE	1480 1480	  .SN ILE A T A T C A	LYS	1600
TACCAACAACG 1460 GLY THR SER ILE	C A T A	T G ASN A A A T P	T A.S. A.S. A.S. A.S. A.S. A.S. A.S.	A A
C A A SER	C II	TGAT TEN LEU	ASN A A A T ASN ASN	GIN C C A A
C A A THR	C A C 0	TACCAATO 1520GLY ASN 1530	C G G LY THR	ILE A A T C
TTACCAACAACG 1460 GLY THR SER ILE	G C	ILE THR ASN ASP ATTACCAATGAT 1520GLY ASN LEU 1530	ILE ASN GLY ASN 1580 1580 THE THE ASN ASN	THR GLU ILE GIN 1640
		<del> </del>	<b>}</b> 1	<u> </u>
CAC		GLY ASN GCAAT )	SER VAL AGCGTT )	ASN ASP AATGAC
CGG 1450		LEU GL) 7 A G G 1510	S SE	Y ASN TAA 1630
TAC		LYS LETA A A A C T	N LYS AAA	ASN GLY
AACATTACCGGCACCT 1450		ALA LYS LEU GLY ASN GCAATA	GLY GIN LYS SER VAL GGTCAAAAAGCGTTA 1570	ASN ASN GLY ASN ASP 1 AATAATGGTAATGACA 1630
A A		AL G C	GE G G	ASI A A

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ILE GLY GLY ASN ILE SER GIN LYS GLU GLY ASNTTGGCGGCAATATCTCGCAAAAGAAGGTAAT 1680 1670 1680	LEU THR ILE SER ASP LYS ILE ASN  C T C A C G A T T C T G A C A A A T T A A T A  1690 ILE THR LYS ARG ILE GLU ILE LYS ALA GLY THR  T C A C C A A A C G G A T A G A A A T T A A G G C A G G T A C T  1740	ASP GIN GLY ASN SER ASP SER GLY VAL GATCAAGGAATTCTGATTCAGGCGTAG 1760 ALA SER ASN ALA ASN LEU THR ILE LYS THR LYSALA SER ASN ALA ASTCTAACCATTAAAACCAAA 1780 1780 1790 1800	GLU LEU LYS LEU THR GLU ASN LEU ASN G A A T T G A A A C C T A A A T A  1820ILE SER GLY PHE ASP LYS ALA GLU ILE VAL ALATTTCAGGTTTTGATAAGCAGAATTGTAGCC1830 1840 1840 1850

### FIG.23J

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GLU GAG

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ASIN A A T

ASIN

ASIN

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	LEU CTA 1980		ASN A A C 2040		
	THR ACA		ASN A A T		
	VAL G T G		ASP 3 A C i		
	ASN A A T 970		SER A G T ( )30		
	HIS C A C		ASN A A T		
	GLY GGT		G G T A		
	ASN A A C		GLU GAA O		
: : : : : :	ALA G C T 196		THR ACT 202	: .	: : :
SER TCA	SER T C T	GLY GGA	ASN A A C	ASN	า ผ
ASP GAT	ILE A T C	ASP GAT	SER A G T	LYS	ር ঘ ঘ
LYS A A A 1940	LYS A A	$\sim$ 1	A C	ALA	2060
VAL G T T	• • •	THR ACA	: : :	ASP C A T	֓֞֝֞֝֞֝֝֓֞֝֝֓֞֝֝֓֓֓֞֝֝
ASN A A T		GLU GAA		ILE	) ¬ <b>⊑</b>
ASN A A C B A B C		VAL GTG		開い	2050
PHE 17 T T 1 19		LYS A A A A 19		LEU	20
THR AAC1		SER		GLY	) פ פ
VAL G T ?		ASN A A 1		ALA	) ט פ
	LYS ASP SER A A A G A T T C A A 1940	ASN GLY HIS ASN VAL THR LEU FAACGGTCACAATGTGACACTA 1970 1980	ASN GLY HIS ASN VAL THR LEU TAACGGTCACAATGTGACACTA 1970 1980	LYS ASP SER  A A A G A T T C A A  1940  LYS ILLE SER ALA ASN GLY HIS ASN VAL THR LEU  A A A T C T C T G C T A A C G G T C A C A A T G T G A C A C T A  1960  SER ASP GLY  T C T G A T G G A A  2000  ASN SER ASN THR GLU GLY ASN SER ASP ASN ASN  A C A G T A A C A C T G A A G G T A A T A G T G A C A A T A A C  2010  2020  2030  2040	LYS ASP SER  A A G A T T C A A  1940   LLYS ILE SER ALA ASN GLY HIS ASN VAL THR LEU  A A A T C T C T G C T A A C G G T C A C A T G T G A C T A  1960  SER ASP GLY  T C T G A T G G A A  2000   ASN SER ASN THR GLU GLY ASN SER ASP ASN ASN  A C A G T A A C A C T G A A G G T A A T A G T G A C A A T A A C   ALA LYS ASN  ALA LYS ASN

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LYS A A A 2100	ALA G C A 2160	SER T C T 2220	SER T C C 2280
HIS CACA	ASN A A T G	LYS A A A	GLU 3 A A '
SER T C T C	ILE A T T A	ILE A T T P	ILE A T T (
THR 3 A C T T 2090	THR A A C C A 2150	GLY F G G A A 2210	LYS A A A A A 270
ILE 'A TCA	THR A CAA	GIN GLY	GLY 3 G T A
ASN ASN ASP AACAACGATA 2080	ASP '	GIN C A A	ASN A A C G
ASN A A C	ALA G C T G	ILE A T C (	ILE A T T A
VAL THR VAL ASN ASN ASP ILE THR SER HIS LYSTAACAGTAAACGATATCACTTCACAAA2070 2080 2100	G T C A G A A A G G A  G T C A G A A A G G A  2120 ILE ASP THR ILE ASN ALA T T G A T A C T A A A G C T G A T A C A A C C A T T A A T G C A  2150  2140  2140	ACTAACAGCTG 2180VAL THR SER ASP ILE GIN GLY GLY ILE LYS SERTAACAAGTGATATCCAAGGTGGAATTAAATCT2190 2200	TATCACAACCA  2240SER THR GLY SER ILE ASN GLY LYS ILE GLU SERGCACAGGTAGCATTAACGGTAAATTGAATCC3250 2250
VAL THR VAL TAACAGTAA	G T C A G A A A G G A 2120ILE ASP THR LYS T T G A T A C T A A A	ALA GCT SER AGT	TATCACAACCA 2240 SER THR GLY SER GCACAGGTAG(
THR A C A	SER GLU CAGAAA 20 ILE ASP TTGATA	A C T A A C A C 2180 VAL THRTAACAA	ILE THR T C A C A 40 SER THR G C A C A 2250
VAL T A 2070	A SER G T C A ( 2120 ILE T T G	A C T A 2180VAL T A2190	T A T C Z 2240 SER G C P
: : :		VAL LYS	
	THR ACTG	VAL G T G	VAL G T A
	ILE A T C A 10	ASN A A C 70	ASP GAT 30
	ASN I AATA 2110	GLY PG G G C A 2170	GLY 7 GGTG 2230
	THR VAL ASN ILE THR ALA ACAGTAAATATCACTGC 2110	THR THR GLY ASN VAL LYS LEU THR ALA A C C A C G C A A C G G G A A C T A A C A G C T G A A C T A A C A G C T 2170 VAL THR SERT A A C A A G TT A A C A A G T2190	ASN SER GLY ASP VAL ASN AATTCTGGTGATGTAAA 2230
	THR ACAG	THR ACC	ASN A A T

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	117/235	
SER T C G 2340	THR A C G 2400	VAL
ACTTACCGCAA 2300THR GLU LYS THR LEU THR VAL GLY ASN VAL SERCCGAAAAACTCTTACTGTAGGCAATGTTTCG	L THR ALA ASN TACTGCAAATA 2360ARG GLY ALA LEU THR THR LEU ALA GLY SER THRGAGGTGCATTAACCACTTTGGCAGGCTCTACG370 2380 2400	Y VAL THR THR TGTAACTACCT 2420SER SER GIN SER GLY GLU ILE GLY GLU GLU
ASN A A T	GLY G G C	GLY
, GLY A G G C 2330	AIA G G C A 2390	GLY
VAL 'GTA	LEU T T G	ILE
THR	THR	GLU
 HR LEU CTCTT 2320	THR A A C C	GLY
A A THR A A C T	 T.A I.EU T A.T.T.A.A 2380	  S
LYS	ASN A A A A AIA AIA	THR TAC(
GLU GAA	ALA GC P GLY G G T	THR ACT
CACTTACCGCAA 2300 THR GLU LYS THR CCGAAAAAC'	VAL THR ALA ASN TTACTGCAAAT 2360ARG GLY ALAGAGGTGCA	ILE ASN GLY THR ASN GLY VAL THR THR A T T A A C G G A C T A A C G G T G T A A C T A C C T 2410 2.SER SER GIN SER
Ö	VAL GTI	G G T
G T A	THR ACT	ASN A A C
A A G T C T G G C T C T G T A A 2290	VAL G T T A 50	THR AACTA
G G C T 2290	GLY ASN THR VGCAACACG	ILE ASN GLY ' TTAACGGGA 2410
T C T	ASN A A C	ASN A A C
A A G	GLY ASN THR VAL THR VAL THR ALA ASN GGCAACACGTTACTGTTACTGCAAATA 2350 2360ARG GLY ALA LEU 2GAGGTGCATT.	ILE A T T
	AUDOTITUTE OUTST	DIU E 26\

G C A TGTT VAL A G GTA VAL AAGACA 開 GGT ACTO

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	118/235		
ALA G C A 2520	THR A C C 2580	GLY G G T 2640	THR A C T 2700
C C C	THR A C C	ASP G A T	LEU
VAL LYS GLY TTAAAGGT C 2510	LEU TTAA	ALA GIN CTCAG	THR ACT(
LYS L A A A 2510	LYS 2 A A A 2570	ALA 1 G C T 2630	GLY A G G C 7 2690
VAL GTT 2	GLY GGCA	SER TCAG	THR ACAG 26
SER LEU THR GCTTAACT( 2500	S既 T C G (	LEU	THR ACT,
LEU TTA 20	SER TCAT	ASP GACC	ASN A A T
THR ALA GLY SER LEU THR VAL LYS GLY GLY ALACTGCCGGCAGCTTAACTGTTAAAGGTGGCGCA2490 2520	GLY THR ALA GGAACTGCAA 2540 THR LEU THR ALA SER SER GLY LYS LEU THR THR CCTTAACTGCATCATCGGGCAAATTAACCACC 25502550	CACTTCAGCCA 2600LYS GLY GIN VAL ASP LEU SER ALA GIN ASP GLYAGGTCAGGTAGACCTTTCAGCTCAGGATGGT 2640	SER ALA ALA AGTGCAGCTA 2660 ASN VAL THR LEU ASN THR THR GLY THR LEU THR . ATGTAACAGTCTCTAACT 2670 2670 2680 2700
ALA GLY SCCGGC	GLY THR ALA GGAACTGCAA 2540 THR LEU THR ALA CCTTAACTGC 2	THR SER ALA A C T T C A G C C A 2600 LYS GLY GIN VAL . A A G G T C A G G T .2610	SER ALA ALA A G T G C A G C T 8660 .ASN VAL THR . A T G T A A C A .2670
ALA G C C	GLY THR GGAACT( 540 .THR LEU .CCTTA?	SER TCAC GLY GGTC	ALA GCA VAL GTA
THR C T (	GLY G G A A 2540 THR C C T	THR A C T T 2600 LYS (	SER T A G T G 2660 ASN Y
• • •	GLU GAA	ILE A T C	ILE ATT
	ALA THR GLU SCGACAGA	ASN A A C	GIN C A A
	ALA G C G 30	ALA SER SER ASN ILE; CTAGCTCAAACAT(2590	ALA GLY GIN ILE CAGGACAAAT 2650
	ASN A T G 2530	SER 8 A G C T 2590	ALA (G C A G 2650
	LYS II.E ASN ALA THR GLUAAAAAATGCGACAGAA2530		SER ILE ALA GLY GIN ILE AGCATTGCAGGACAAATT 2650
	LYS A A A A	GLU GAG	SER A G C

	119/235		
THR VAL GLU GLY SER SER ILE ASN ALA ACCGTAGAGGTTCAAGCATTAACGCAA 2720ASN GLU GLY THR LEU VAL ILE ASN ALA ASN ASPASN GLU GLY THR LEU VAL ILE ASN ALA ASN ASPACGAAGGCACCTTGGTTATTAACGCAAACGAC	SER GLY A T C A G G T A ARG THR GLU VAL ASN ALA THR ASN ALA SER C G T A C A G T A A A T G C A A C T C A A G C 2820	GLY SER GLY SER VAL THR ALA LYS THR GGCTCTGGTAGCGTGACTGCGAAAACCT 2840SER SER SER VAL ASN ILE THR GLY ASP LEU ASNCAAGCAGCGTGAATATCACCGGGGATTTAAACCAAGCAGCGTGAATATCACCGGGGATTTAAAC	THR ILE ASN GLY LEU ASN ILE ILE SER A C A A T A A A T A T C A T T T C G G 2890
ILE ASN ALA LATTAACGC 7 2720ASN GLU GLYACGAAGGC	ALA SER GLY GCATCAGGG 2780ASN ARG THRACCGTACA	ALA LYS THR GCGAAAACC 2840SER SER SERCAAGCAGC	ILE ILE SER ATCATTTCG 2900
SER ] A A G C A 272A	LYS A G G 278 278 278	THR P 284 284S	ASN I AATA 290
GLY SER 3 G T T C A A 0	ASP GLY ATGGT	SER GLY SER VAL THR CTGGTAGCGTGAC 2830	SLY LEU GGTTA1
VAL GLU G 3 T A G A G G 2710	LEU PG TAG 2770	GLY S T G G T A 2830	ASN GLY A A T G G G 2890
THR VALACGT	ALA LYS LEU GCCAAGTTA 277	GLY SER	THR ILE ACAATAA

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	120/235		
GLY G G C 2940	GLU G A A 3000	ALA G C T 3060	THR A C A 3120
ARG A G A	ILE A T T	THR LEU	ASN THR AACAC 3120
ARG LEU GCTTA 1 30	VAL G T A A	THR ACA	VAL GTT
ARG 3 C G C 2930	GLU A G A A G 2990	ARG GLU GAGAAA 3050	; THR TACG 3110
VAL	GLU		VAL ARG PHE  FGTACGTTTTA 3080ILE GLU PRO ASN THR ILE THR VAL ASN THRTTGAACCAAATAATACCATTACGGTTAACACA3090 3100 3120
THR ACTO	VAL G T A G	 5 ASP GLU GLU 3.A T G A A G A A A 3040	THR A C C
ARG ASN GAAACA 2920	SER AGTG	GLU GAA	ASN A A T
ARG P A G A A 2920	 C ALA S G C A A 2980	 G ASP G G A T G	 A ASN P A A T A 3100
GLY GGT	LYS GLU ILE GLU VAL LYS TYR ILE GLN A A G G A A A T A T A T C C A G C 2950PRO GLY VAL ALAC A G G T G A A T A T A T C C A G C	ALA LYS ARG VAL LEU GLU LYS VAL LYS  3 C G A A A C G C G T C C T T G A G A A G T G A A A G  3010 ASP LEU SER ATTTATCTG	LYS LEU GLY VAL SER ALA VAL ARG PHE A A A C T T G G T G T A A G T G C T G T A C G T T T T A 3070ILE GLU PRO ASN 33090 33090
ASN AATG	TYR ILE A T A T A T C ( 2960PRO GLY C A G G T (	LYS VAL 3 A A A G T G A 3020ASP LEU A T T T A T	VAL ARG FGTACGTT 3080ILE GLUTGAAC
GLU A A A	A T A T 2960 PRO C A (	G A A A (3020 ASP A T 5 3030	T G T A C 3080 ILE T T G T T G
	LYS A A A P	GLU GAG	ALA G C T
	VAL G T G i	LEUCTT	SER AGT(
	GLU GAG	VAL GTCO	VAL GTAP O
	ILE CATTG 2950	ARG V C G C G 3010	GLY VG GG TG 3070
	LYS GLU ILE GLU AGGAAATTGAGO 2950	ALA LYS ARG CGAAACGCO	LYS LEU GLY AACTTGGTG 3070
	LYS A A G	ALA 3 C G .	LYS A A A A

# FIG.23P

			CYS	T G T	3180				* *	T A G	3240
			SER GLN VAL THR ILE SER GLU GLY LYS ALA CYS	GTCAAGTGACAATTTCTGAAGGTAAGGCGTGT					CYS THR ASN VAL ALA ASP ASP GLY GLN GIN ***	GTACCAATGTTGCTGACGATGGACAGTAG	
			LYS	AAG					CIN	CAG	
			GLY	GGT	170				GLY	GGA	3230
			CITO	3 A A (	3170				ASP	GAT (	, co
			SER	I C I					ASP	3 A C (	
			II.E	A T T	0				ALA	C T (	0
:	A	:	出	A C A i	3160	:	-:-	:	VAL	STT(	3220
贸	TCA		VAL	G ∏ G		VAL	GTA		ASIN	A A T	
R2	CCA		GIN	CAA(		ALA	GCA		强	A C C i	
THR ARG PRO SER	AAAATGAGTTTACAACCAGACCATCAA	3140	殿.	GT (	3150	GLY ALA ALA VAL	GGCGCAGCAGTAT	3200	.CYS	GT.	3210
置	ACC.	m	:	:	•	GLY	0 0 0	m	:	:	:
置	ACA.					ASIN					
GLN ASN GLU PHE THR	T T T	0				PHE SER SER GLY ASIN	TCTCAAGTGGTAAT	0			
OTN CITI	GAG	3130				SE	AGT	3190			
ASIN	AAT					SES	TCA				
SIN	AA					出	J L				

# FIG.24A

PMH1 hnw1A sequence

	122	/235						
	VAL ASN ILE VAL LYS GLY THR GLU LEU GLN ASN TCAATATGTTAAAGGAACCGAATTACAGAAT	09				ILE	АТТ	
	VAL ASN ILE VAL LYS GLY THR GLU LEU GLN ASN TCAATATGTTAAAGGAACCGAATTACAGAA					GLU LYS LYS ASN ALA PRO THR LYS THR ILLE	AGAAAAGAATGCCCCTACCAAGACTACAATT	
	LEU T T A					混	ACT	
	GLU GAA	20				LYS	AAG	-
	THR A C C					强	ACC	
	GLY G G A					PRO	$\mathbb{C} \subset \mathbb{T}$	
	LYS A A A	10				ALA	ລ ລ ອ	1.1
: : :	VAL G T T	7	:	:	:	ASIN	AAT	1.11.
ASN A A T	ILE A T T		ILE	ATT		LYS	A A G	
ASP G A T	ASIN A A T		SER	AGT		LYS	AAA	
PRO C C G 20	VAL	30	ASP	GAT	80	GIU	. A G	1313
ASP G A C	• •	•	GLY	0 0 0		:	i	
LEU TTA			ARG	A G G				
LEU 3 T T G			VAL	GTT	70			
LYS GLU TRP LEU LEU ASP PRO ASP ASN A A A G A G T G G T T G T T A G A C C G G A T A A T G 10 20			ASP LEU VAL VAL ARG GLY ASP SER ILE	GATTTGGTTGTTAGGGGCGATAGTAG				
GLU 1 G A G			EE I	TTG				
LYS A A A			ASP	GA T				

4B

ACG G G T 290 ΤV Ø ASN GLY 园 LL Ø V Ø 园 ် ဗ AA TGGA TCAGAA GE 閉 GLY ASN 段 AA GGT G T T TAT ACC ⊱ IIE ... A T A T T *I* AAC GAT  $\vdash$ ATGTT ATT ACA ... ASIN TGGGTT ...ASN ACT GAA 混 E E TRP S S ⊱ WAL VAL G T G ď ⊏ K ⊱ ASIN ZTO UTA GLY TGG AGG Ø Ø 190 Ø WAL ر ن ق ₽ Þ G G AAA A A Ø LYS K AAT Ø  $\vdash$ ASN Ø  $\vdash$ 

123/235

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T G 360 ₽ L GGT G A G 350 GLU 0 C CACTT ď Ç ⊱ Ø AAT ASIN  $\dots$  A T A A A SIH:..

: G TTC GATATCGCC ⊱ GLY \_ G  $^{\circ}$ SE C ⊱ ₽  $\mathcal{O}$ Ø 亡  $\vdash$ ASN Ø

124	/23	35
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	124/235	
GLU LYS GLY ASN ASN LEU THR ILE THR ALA GLN A A A A A G G T A A T A A T C T A A C C A T T A C C G C T C A A 390 420	N LYS ASP GLY TAAAGACGAA 440LYS GIN LEU ARG LEU ASN ASN VAL SER LEU ASNAACAACTTAGACTTAATAATGTATCTTTAAATA450 440	U ASN PHE ILE A A A C T T T A T T G 500ALA ASN GIN ASN PHE THR HIS ASN ILE SERC A A A T C A A A T A A T T T T A C A C
ALA G C T	LEU T T A	ILE A T T
THR ACC	SER T C T	ASN A A C
ILE A T T 410	VAL G T A 470	HIS CAC 530
THR A C C	ASN A A T	THR A C A
GLU LYS GLY ASN ASN LEU THR ILE THR ALA GLN A A A A A G G T A A T A A T C T A A C C A T T A C C G C T C A A A S S S S S S S S S S S S S S S S	N LYS ASP GLY TAAAGACGGAA 440LYS GIN LEU ARG LEU ASN ASN VAL SER LEU ASNAACAACTTAGACTTAATATGTATCTTTAAA	U ASN PHE ILE A A A C T T T A T T G 500 ALA ASN GLN ASN PHE THR HIS ASN ILE C A A A T C A A A T A A T T T T A C A C
ASN A A T 00	A C T T 460	. ASN TAAT 520
ASIN A A T 4(	 A ARG A G A 46	 G ASN A A T 52
G G T	GGA LEU CTT	ILE A T T GIN C A A
LYS A A A	ASP G A C GIN C A A	PHE TTT ASN ASN
GLU A A 390	IN LYS  T A A A 440 LYS A A A 50	TU ASN S A A C S 500 AIA C A P
: : :	ASN A A T	TTA T
	SER T C T	GLY GGT
	THR A A C C 430	ALA G C A O
	ILE ATA 43	GLY 7 G G T G 490
	GLY ASN ILE THR SER ASN LYS ASP GLY GAAATATAACCTCTAATAAGACGGA 430LYS GIN LEUAACAACTTAACAACTT	GLY THR GLY ALA GLY LEU ASN PHE ILE GGAACAGGTGCAGGTTTAAACTTTATTG 490ALA ASN GLN ASNCAAATCAAAA'
	GLY ASN ILE THR SER ASN LYS ASP GLY  GGAATATAACCTCTAATAAGACGGAA 430LYS GIN LEU ARGAACAACTTAG	GLY G G A

TCCGGAGTAGTAA... 560 SER ILE ASIN IE 909099 ALA

3 A T T A A C A 550

A A G 600 GCT . A A A A A C ( 590 ASIN AAA CAAACTACG 580 GLN ... CGATTAAT ASIN

	ASP	GAT	099				SES	T C A	720				GLY	G G T 780			
	SER ASN	AAT					ASP	GAT					ILE	ATT			
	SER	GGAACGTATCTACTCTTACTTTAAGCAATGAT					S S	A C A G C A A T C A T T C G A C A A A C T C C A G T G A T T C A					ASN GLU MET LYS PHE ASN ILE	G C A A G A A T G A A A T G A A A T T T A A T G G T 750 750 750			
	LEU	TTA	650				ASN SER	TCC	710				盟	T T T 770			
	訊	ACT					ASIN	AAC					LYS	A A A			
	THR LEU THR LEU	СТТ					SER THR	ACA					MET	ATG			
	当	ACT	0;				S S S	TCG	0				CIN	G A A 0			
: :	: SE	TCT	640	:	 G	:	HIS	CAT	700	:	.: G::	•	ASN	A A T G 760		A	:
TYR T A C	VAL	GTA		VAL	GTC		ASIN	AAT		HIS	CAC		ASIN	A'A T	1 54	T T A	
SER T C T	ASIN	AAC		TYR	TAT		SER	A G C		出	TTC		LYS	A A G	, כם ל	ANG A G G	
TYR ASP SER TYR TATGACTCTTACT	620 TRP ASN VAL	G	630	ILE LYS TYR VAL	ATTAAATATGTCG	089	ASP SER ASN HIS	. A C	069	VAL LYS PHE HIS	GTAAAGTTCCACG	740	GLY LYS ASN	G C	191 79% 3Hg 1117	GLO FRE ARG LEU GAATTTAGGTTAA	800
	:	:	:	IE	ATT		•	:	:	VAL	GTA		:	: :	11	G A A	
SER AGC				出	T $T$ $T$					GLY	G G A					ALA G C T	
THR ACA/	610			開	ACC	0,				ALA	S C G	0			7 77	LYS A A G (	0
ASN A A T	61			出	T $T$	0/9				出	TTT	730				ALA G C C	790
TRP TGG				LYS	AAA					SES	AGT				£	ASIN A A T (	
ALA TRP ASN THR SER GCATGGAATACAAGC				ALA	GCGAAATTTACCTTT					ARG	CGAAGTTTTGCGGGA				£	ASIN ASIN ALA LIS ALA AATAATGCCAAGGCT	
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PRO C C A 840	ASP G A T 900	SER I C T 960	ASN A A T 1020
ARG A G A (	PHE I T C (	VAL 3 T T '	ILE ATCA
ASN A A C A	PHE I'T'T'T	ASN A A C (	GLU G A A A
PRO C C T A 830	VAL G T G 1 890	ILE A T T 7	PHE   T T C
班 A C T C	SER T C T (	SER ICAA	ALA 3 C T 1
THR A	GLY GGT'	ASP GATT	ASN A A T G
J LYS ' G A A G A 820	GLY G G A (	MET A T G (	TYR T A T 7
GLI A	SER ASN ILE TCTAATATTT 860 SER VAL THR GLY GLY SER VAL PHE ASP CGGTCACTGGCGAGGTTCTGTGTTTTCGAT CGGTCACTGGCGAGGTTCTGTGTTTTCGAT 870	GLY LYS GLY  GG T A A A G G G A  920  THR GLU LEU LYS MET ASP SER ILE ASN VAL SER  C T G A G C T A A A G A T G G A T T C A A T T A A C G T T T C T  950	LEU ASN SER TTAAATTCCC 980HIS VAL ARG LYS TYR ASN ALA PHE GLU ILE ASN ATGTTCGCAAGTATAATGCTTTTGAAATCAAT A990 1000 1000
ASN A A T G	SER ASN ILE TCTAATATTT 860 SER VAL THR GLY . CGGTCACTGG	GLY LYS GLY GGTAAAGGGA 920THR GLU LEU LYSCTGAGCTAAAG	LEU ASN SER T T A A A T T C C C 980 HIS VAL ARG LYS . A T G T T C G C A A . 990
PRO C C A A	ASN AATA VAL GTCA	GLY LYS GLY GGTAAAGG( 920THR GLU LEU CTGAGCTA	LEU ASN TTAAAT7 980HIS VAL ATGTTC
LYS A A (	SER 1 T C T A 860 SER C G G R70	GLY G G T 920 THR	LEU T T A 980 .HIS . A T
• • •	LEU TTA	TRP T G G	理R A C C :
	PHE TTTT	LEUCTT	LEU CTT
	GIN TCAGT 850	A ASN TAAC 910	TAAT 970
	PRO ILE CAATT (	ALA G C T 93.	SER TCT 97
	LEU PRO ILE GIN PHE LEU CTACCAATTCAGTTTTTA 850	ILE TYR ALA ASN LEU TRPATATAGCTAACCTTTGG910	SER GLY SER ASN LEU THR AGCGGCTCTAATCTTACC 970
	LEU CTAC	ILE A T A	SER A G C

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127/235		
GLY G G C 1140	11.E A T C 1200	
LEU TTG	ILE	
ILE A T C	ILE A T C	
SER T C C 1130	ASN A A T 1190	
ILE ATA 1	GLY GGGG	
ASN A A C	MET A T G	
HIS CAC 20	ILE ATT 80	
 THR A C C	 T SER 11	: : :
ALA GCC SER	ASN A A C SER A G C	GLU S G A A
ASN FAAT ASN ASN	GIN A C A A SER A A G C	THR LEU GLU ACGCTAGA 220
ASN 1100 ILE	GLY C G G 7 1160 SER	THR LEU GLU TACGCTAGAAG
	~_	
TYR 3 T A (	LEU ICT(	ASIN A A A
C G G (0)	C A C '	A ALA : A G C . 1210
T A ASN	CGT	A G C
T C G	C A A	LYS ARG ALA ALA ASN VAL A A G C G A G C A A A T G T 1210
PIE	G G	LYS A A
	ASN ASN ALA  CAATAATGCCA 1100ILE ASN SER THR HIS ASN ILE SER ILE LEU GLYTCAATTCAACCCACAACATATCCATCTTGGGCTCAATTCAACCCACACATAT130 1120 1120	S ASN ASN ALA  C A A T A A T G C C A  1100   ILLE ASN SER THR HIS ASN ILE SER ILE LEU GLY  T C A A T T C A A C C C A C A A C A T A T

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	128/235		
LYS A A G 1260	GLU G A A 1320	THR A C C 1380	ILE A T A 1440
ASP ASN VAL 3 A C A A C G T A A	C G C	LYS A A A A	ASN A A T
ASN A A C	ILE A T T	GLY 3 G A	ILE ATTA
ASP C A C 1250	SER LEU ILE AGTTAATTG 1310	PHE LYS GLY TTAAAGGAA 1370	ALA GLU ; C C G A A A 1430
SER ICTG 12	SER AGT	PHE 17 7 7 7 1	ALA 3 C C C
ASIN A A T T	LEU FTA i	ILE ATCT	THR ACTG
SER HIS GTCACA 1240	ASN A A T ?	ALA 3 C C A	GLY
SER H A G T C 1 1240	 A GLY AS 3 G G A 7	 GLU P 3 A A G 1360	 T ASN G A A T G
ASN A A T i	LEU TTG7 GLU GLU	SER I C C i LYS A A A C	ASN A A C 7 ASN
ALA ASP ASN SER HIS ASN SER ASP ASN VAL LYSCCGATAATAGTCACAATTCTGACAACGTAAAG	TGGCAACTTGA  1280THR VAL GLU GLY ASN LEU SER LEU ILE GLY GLUCCGTTGAGGGAATTTAAGTTTGGCGAA 1320	ASN LEU SER CAATCTCTCCA 1340ILE GLU LYS GLU ALA ILE PHE LYS GLY LYS THRTGAAAAGCCATCTTTAAAGGAAAACC 1350 1360 1360	THR GLY ASN CACCGGCAACT 1400PHE THR ASN ASN GLY THR ALA GLU ILE ASN ILETACCAATAATGGCACTGCCGAAATTAATA 1440 11410
ALA C C (	J GLY T G G C 1280 THR C C (	ASN C A A T ( 1340 ILE T T (	THR C A C C ( 1400 PHE T T P
: : :		<u> </u>	ILE A T C A 1 
	ASN A A T C	ASN A A C G	ASN A A C A
	ILE ATAA O	ILE ATTA O	LEU C T A A O
	ASP ARG THR ILE ASN LEGGATAGACTATAAATCT 1270	ASN ALA ASN ILE ASN GL) A A T G C A A T A T T A A C G G 1330	LYS ASP SER LEU ASN ILE THR GLY ASN A A G G A C A G C C T A A A C A T C A C G G C A A C T 1390PHE THR ASN ASNT T A C C A A T A A C A T A A C A T A A C A T A A C A T A A C A T A A C A T A A C A T A A C A T A A C A T A A C A T A A C C A A T A A C A C
	ARG A G A	ALA G C A	ASP G A C ,
	ASP GATA	ASN A A T	LYS A A G

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		129/235		
	THR A C T 1500	ASN A A T 1560	GLN 2 A A 1620	
	THR ACCA	GLY 3 G G 7	SER CGC	
	ILE '	JIN A A G	ILE NTCT	
	ASN 1 A A C A 190	ILE ASN LYS GIN TTAACAAACAAC	ASN 1	
	U ASN A A A 1490	N LYS C A A 1550	Y ASN CAA'	
	LYS LEU AATTAP 14	ASI A A A A	GLY GLY 3 G C G G C A	
	LYS A A A	ILE A T I	GLY G G C	
	GLY 3 G C 0	ILE A T A A 0	ILE ATTC	
:	ASP (3 A T G 1480	A ASP J 3 A T A 1540	 G GLU 1	
BAT	ASN 1 A T (	ILE ATTA GLY G A (	ASN AAT ( ILE ATT (	SER PCT
TCTTGGCGATA	1460 ILE THR ASN ASP GLY LYS LEU ASN ILE THR THR TTACCAATGACAAATTAAACATCACCACT	N LYS SER ILE AAAAAGCATTA 1520ILE ARG GLY ASP ILE ILE ASN LYS GIN GLY ASNTCCGCGAGATATAATTAACAAGGGAAT 1540 1540 1550	TAATAGTAATG  TAATAGTAATG  1580 ALA GLU ILE GLU ILE GLY GLY ASN ILE SER GIN CTGAAATTGACGCGCAATATCTCGCAA  1620  1620	SER FCT1
T T	1460 ILE T T A	N LYS A A A A A A 1520ILE T C C	ASN T A A T 7 1580 ALA C T C	ILE C A T T T 1640
	1460 ILE T			LYS GLU GLY ASN LEU THR ILE SER SER A A A G A A G G T A A T C T C A C C A T T C T C T G 1630
A G C C A A G G A G T G G T A A G		HIS ALA LYS SER GLY GIN CACGCCAAGAGCGGTCA 1510	LEU ASN ILE THR ASPAST TTAAATATTACGGACAA 1570	ASN LEU THR A T C T C A C (
l G G		ΕΗ C C C	で り り り り り り り り り り り	SN J
A G	1450	S S S A G A G A G 1510	E T	Х А ; ТА. 1630
G G	<del></del>	ALA LYS 3 C C A A G P 1510	ILE A T	GEN G G
CAA		ALA G C C	LEU ASN ILE THR TAAATATTACGO 1570	LYS GLU GLY AAGAAGGTA 1630
A G C		HIS C A C C	LEU TTA	LYS A A A
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ILE A T C 1680	THR A C C 1740	ALA G C A 1800	SER A G T 1860
ASP LYS VAL ASN ILE THR LYS GIN ILE THR ILEATAAAGTCAATATTACCAAACAGATAATC1650 1660 1660 1670	GLU SER SER  3 G A G A G T T C T A  1700  SER SER SER THR ALA SER ASP ALA ASN LEU THR  G T T C A A G C A A G T G A T G C C A A T C T A A C C  G T T C A A G C A A G T G A T G C C A A T C T A A C C  G T T C A A G C A A G T G A T G C C A A T C T A A C C  G T T C A A G C A A G T G A T G C C A A T C T A A C C  G T T C A A G C A C A G C A A G T G A T G C C A A T C T A A C C  G T T C A A G C A C A G C A A G T G A T G C C A A T C T A A C C  G T T C A A G C A A G T G A T G C C A A T C T A A C C  G T T C A A G C A C A G C A A G T G A T G C C A A T C T A A C C  G T T C A A G C A C A G C A A G T G A T G C C A A T C T A A C C	THR LEU THR  A C A T T A A C A G  1760  ASP ASN LEU ASN ILE SER GLY PHE ASN LYS ALA  A C A A T C T A A C A T T T C A G G T T T T A A T A A G C A  1800  1170	ASN SER ASP  A A C A G T G A T T  1820   LEU ILE GLY LYS ALA SER SER ASP ASN SER  T A A T T A T T G G C A A G G C T A G C A G T G A C A G T  1830  1840  1860
ILE A T A A	ASN A A T C	ASN AATA	SER ASP GTGACA
S GIN A C A G P 1670	P ALA TGCCA 1730	PHE FTTP 1790	SER YAGT 1850
THR LYS	ASP GATG	GLY G G T	SER SER 1818
THR	SER A A G T G	ILE SER GLY TTTCAGGTT	ALA G C T A
ASN ILE ATATTA 1660	  IR ALA 1720	  ILE A C A T T 1780	
ASN C A A C	SER C T A SER THR G C A C A (	 A G ASN A A A C A	ASP 3 A T T ILE GLY 1 T G G C A
VAL GTCP	SER SER SER	THR LEU CTP	ASP GA7 ILE ATT
LYS A A A G	SER AGTT SER TCAP	THR LEU CATTA? 60 ASP ASN A CAATC	SER AGT( ILE ATTP
ATP	LYS ALA GLY VAL ASP GLY GLU SER SER A A A G C A G G C G T T G A T G G G G A G A G T C T A  1690SER SER THRG T C A A G C A C I	ILE LYS THR LYS GLU LEU THR LEU THR ATTAAACAAGTTAACATTAACAG 1750ASP ASN LEU ASN ASN 1770	GLU ILE THR ALA LYS ASP ASN SER ASP GAAATTACAGCTAAAGATAACAGTGATT 1810LEU ILE ILE GLYTAATTATTGG
• • •	G C C C C C C C C C C C C C C C C C C C	LEU TTA	ASP G A T
	ASP G A T	CIU GAGI	LYS , A A A G
	N VAL 3 C G T T 1690	LYS (A A A B B B B B B B B B B B B B B B B	ALA G C T LO
	ALA GLY VAL ASP GLY 5 C A G G C G T T G A T G G 0 1690	LYS THR I AAAACCA 1750	ILE THR ALA TTACAGCTA 1810
	ALA G C A	LYS A A A	ILE A T T
	LYS A A A G	ILE A T T	GLU GAAA

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131/235 AAT AACGGT 2040 ₽ ASIN SER G K G G A E GLY ASN Z, AGCACC CGGTA 黑 WAL 2030 贸 開 Ø Ŋ TA VAL G G E ASP ASP G A ø AAG 1900 ں Ŗ LYS Α... Ä G Ø ACT Ø E Ø ASIN ALA G A . ဗ AA TTA  $\Gamma$ T G ⊱ 段 国 Ŗ  $\vdash$ G <u>ဗ</u> AGCAAA ATCGGC ..1890 图::: LYS ]]] GLY 段 E 드 ASIN ASSIN K ø Z, K Ø GACAAC EDI ASN CAC ASP Ø ΑT Ø WAL G C H  $\mathcal{O}$ ASN A G Ø

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	132/235		
ALA G C A 2100	11.E A T T 2160	VAL G T T 2220	ASN A A T 2280
LYS A A A G	ASP GATP	LEU THR PTAACT	THR GLY
THRACT	G G C	LEU T T A	THR ACA
ILE THR THR TCACTACT? 2090	THR A A C A 2150	ASP 2 G A T 2210	ALA 2 G C A 2270
ILE	LYS A A A A	GLY G G C	THR ACC
SER ALA SER GLU GLY GLY ILE THR THR LYS ALA CTGCATCAGAGGTATCACTACTAAGCAG2070 2080 2100	THR THR GLY 3 A C C A C A G G T A 2120 SER VAL GLU VAL THR ALA LYS THR GLY ASP ILE G C G T G G A A G T A A C T G C T A A A C A G G C G A T A T T 2130 2140 2150	LYS THR VAL  LAAGACAGTAA 2180 SER VAL THR ALA SER THR GLY ASP LEU THR VALGTGTTACAGCAAGCACTGGCGATTTAACTGTT2190 2210	SER ALA THR  LAGTGCGACAG  2240  GLU GLY ALA ALA THR LEU THR ALA THR GLY ASN  AAGGAGCTGCAACCTTAACCGCAACAGGGAAT  AAGGAGCTGCAACCTTAACCGCAACAGGGAAT  2250
LU GLY A A G G A 2080	THR ACT	  SER C A A G C 2200	THR ACC 60
GLU AGAP 20	 VAL 1 G T A A 2140	LYS THR VAL  LAAGACAGTAA 2180  SER VAL THR ALAGTGTTACAGCAA21902190	 AG ALA IGCAA 2260
SER	GLY A G G 7 GLU GLU F G A P	VAL NGTA THR	THR 3 A C A ALA G C T
ALA GCP	THR ACA VAL GTG	LYS THR VAL AGACAGT? 80 SER VAL THR GTGTTAC?	SER ALA GTGCGA 40 GLU GLY A A G G A G 2250
SER C T	G A C C A 2120SER G C G	LYS r A A G 2180 SER G T C T	SER ALA THR TAGTGCGACA 2240GLU GLY ALA A A G G A G C 5
	ALA GCC	SER GLY CCGGT	ILE ATT
	ASN AATC	SER TC	THR. A C C
	R ILE C A T T A 2110	ILE ATTT 70	A ALA CTGCA 2230
	THR THR CAACCI	THR 'A C G 21	ALA G C T 22
	GLY THR THR ILE ASN ALA THR THR GLY GGCACATTAATGCGACCACAGGTA 2110SER VAL GLU VALGCGTGGAAGT	SER GLY THR ILE SER GLY LYS THR VAL AGCGGTACGATTCCGGTAAGACAGTAA 2170 2180SER VAL THR ALAGTGTTACAGC	ARG LYS ALA ALA THR ILE SER ALA THR A G G A A A G C T G C A A C C A T T A G T G C G A C A G 2230GLU GLY ALA ALA ALA ALA ALA ALA ALA ALA ALA A
	G C C A	SER A G C	ARG A G G

	A.				_					<b></b>		r (Ri	 06	
THE	ည ည						ALA	L J					GLY	C G
PEG-	T T G						GIN	CAG					GLY THR	ACC
開	ACT	2290					ALA GIN ASP	GAT	2350					T T A
出	ACT	90					GLY	GGT	20				出	ACT
GLU	GAA						段	AGC					開	ACT
ALA	ACCTTGACTACTGAAGCCGGTTCTAGCA		•	٠	•		IE	GCTCAGGATGGTAGCATTGCAGGACAAA		•	•	•	VAL	GGCACCTTAACTACTGTAGAAGGTTCAA
GLY	GGT	2300	HE:	. T C	2310		ALA	GCA	2360	ILE	T T	2370	CIFU	GAA
ALA GLY SER SER	$T \subset T$		ILE THR SER THR LYS GLY GLN VAL ASP LEU SER	TCACTTCAACTAAGGGTCAGGTAGACCTTTCA			ILE ALA GLY GIN	G G A		ILE SER ALA ALA ASN VAL THR LEU ASN THR THR	TTAGTGCAGCTAATGTGACATTAAATACCACA		VAL GLU GLY SER	G G T
SER	AGC		段	T C A			GIN	CAA		ALA	GCA		SE	T C A
:	A	:	黑	ACT	2320		:	Α	:	ALA	GCT	2380	:	A
			LYS	AAG	0;					ASN	AAT	02		
			GLY	GGT						VAL	G T G			
			GIN	CAG	(1					開	ACA			
			VAL	G T A	2330					国	TTA	2390		
			ASP	GAC						ASIN	AAT			
			E	C T T		•				出	ACC			
			SES	TCA	2340					開	ACA	2400		
									-					

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, G C T A T T 2460 ALA 园 AAGGCAACCAGTGGCACC 2440 2450 强 GLY 贸 開 ALA LYS ... ACATT HE ...ASIN

2420

2410

Α. GGT GCTAAGCTAGAT 2480 ASP 国 LYS ALA 1 A A A G A C C 2470 ASP LYS AACGCA ALA ASIN

# FIG.24N

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	134/235		
ALA G C A 2520	GLY SER VAL GGTAGCGTGA 2540 THR ALA LYS THR SER SER ASN VAL ASN ILE THR: .CTGCGAAACCTCAAGTAATGTGAATATCACC .2550	ASN GLY LEU A A T G G T T A A 2600 ASN ILE ILE SER GLU ASN GLY ARG ASN THR VAL ASN ILE ILE SER GLU ASN GLY ARG ASN THR VAL ASN 12610 2620 2640	GLU G A A 2700
ASN A A T	ILE A T C	THR	VAL G T A C
VAL G T A A	ASN A A T A	ARG ASN 1 G A A A C A	SER AGCG
GLU 1 G A A 2510	VAL 1 G T G 7 2570	ARG 7 A G A 2630	VAL ALA 3 T A G C A A 2690
THR ALA SER GLY ASN ARG THR GLU VAL ASN ALACGGCATCAGGTAACCGTACAGAAGTAAATGCA2490 2500 2500	ASN AATG 25	GLY GGTA	ILE ASP VAL A T T G A T G T G A 2660 LYS TYR ILE GIN PRO GLY VAL ALA SER VAL GLU . A A T A T A T C C A A C C A G G T G T A G C G T A G A A 2670 2670 2700
ARG C G T	SER AGTA	ASN A A T C	PRO GLY
ASN AACC DO	SER TCAA	GLU G A A 7 20	PRO C C A
GLY 7 G G T. A 2500	VAL 3 T G A LYS THR S A A A A C C T 2560	 SER C T C G G 2620	 A GIN E C A A C 2680
SER T C A G	GLY SER VAL GGTAGCGTGA 2540 THR ALA LYS THR . CTGCGAAAAC	ASN GLY LEU A A T G G G T T A A 2600 ASN ILE ILE SER . A T A T C A T T T C C 2610	ILE ASP VAL A T T G A T G T G A 2660 LYS TYR ILE GLN . A A T A T A T C C A
ALA G C A T	GLY SER GGTAGC( 540 THR ALA . CTGCG?	ASN GLY A T G G G 00 ASN ILE A T A T C 2610	ASP GAT TYR TAT
THR C G G	GLY G G T A 2540 THR C T G		ILE A T T 2660 LYS A A 2670
• • •	SER T C T	ILE ATA	GLU G A A
	G G T	THR A C A A	LYS A A G
	SER A G T G 30	SER A G C A 90	GLY G G C 50
	ALA S G C A A 2530	LEU (17 T A A 2590	ARG G A G A G 2650
	THR ASN ALA SER GLY SER A CTAACGCAAGTGGTTCT 2530	GLY ASP LEU SER THR ILE GGGGATTTAAGCACAATA 2590	ARG LEU ARG GLY LYS GLU CGCTTAAGAGGCAAGGAA 2650
	THRACTA	G G G G	ARG C G C

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VAL LEU ... GICCIIG...

C G C

GAAGCGAAA

GLU VAL ILE GAGGTAATT

### FIG.24N

	135/235		
ARG	ILE	GLU	
A G A	A T T	G A A	
2760	2820	2880	
GLU GAA	PRO ASN ASN ALA CAAATAATGCCA 2810	SER TCT(	
GLU	ASN	ILE	
GAA	A A T	A T T	
ASP	ASN	ILE	
r G A C	A A A T	3 A T A	
2750	2810	2870	
SER	PRO	VAL	
TCT	C C A	GTG	
LEU	GLU	GLN	
TTA	GAG	C A A	
ASP	VAL	SER	
GAT	GTT	AGT	
2720 GLU LYS VAL LYS ASP LEU SER ASP GLU GLU ARG AGAAAGTAAAGATTTATCTGACGAAGAAGA 2730	GLY VAL SER  IGGTGTAAGTG 2780ALA VAL ARG PHE VAL GLU PRO ASN ASN ALA ILECTGTACGTTGAGCCAAATAATGCCATTC790 2820	GLU PHE THR  T.G.A.A.T.T.A.C.A.A 2840THR ARG PRO SER GIN VAL ILE ILE SER GLUC.C.A.G.A.C.G.T.C.A.A.G.T.C.A.A.T.T.T.C.T.G.A.A. 2850 2850	: : :
VAL G T A	GLU THR LEU ALA LYS LEU GLY VAL SER GAAACTAGCCAAACTTGGTGTAAGTG 2770ALA VAL ARG PHECTGTACGTTT	THR ILE ASN THR GIN ASN GLU PHE THR ACGATTACACACAAATGAATTACACAA 2840THR ARG PRO SERCCAGACGTC	GLY LYS ALA CYS PHE SER SER GLY ASN GGTAAGGCGTGTTTCTCAAGTGGTAATG 2890 2890
LYS A A A	GLY VAL SER GGTGTAAGT 180 ALA VAL ARG CTGTACGT	GLU PHE THR 3 A A T T T A C 1 340 THR ARG PRO C C A G A C C G 2850	GLY G G T
2720 GLU A G 7	T G G T 2780 ALA C T 0	GLU T G A A 2840 THR C C	SER AAGT 2900
	CIT	ASN A A T	SER T C A
	LYS	GIN	PHE
	A A A A	C A A	TTCT
10	GLU THR LEU ALA LYS LEU	THR ILE ASN THR GIN	GLY LYS ALA CYS
	AAACACTAGCCAAACT	CGATTAATACACAA	GTAAGGCGTGTT
	2770	2830	2890
2710	LEU	ASN 7	ALA
	CTA	A A T A	G C G
	27	2830	28
	THR	ILE	LYS
	ACA	ATT	A A G
	GLU	THR	GLY
	GAA	A C G	GGT

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AAT ASIN GTATGT WAL ... G C G C A G C A 0

> GLY GLN PRO \*\*\* GGACAGCCGTAG 2950

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PMH1 hmw2A sequence

G A ⊣ G A 0000 GAC ASP Ø E E L G 国 <del>[--</del>1  $\vdash$ G 136 G ⊱ A G G Ø AA

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	ILE A T C 240	ILE A T T 300	VAL G T T 360	
	ASN A A T A	LYS A A G <i>i</i>	TRP T G G	
	ILE A T C A	VAL 3 T T ?	SER GLY GCGGC1 50	
	ASP G A C <i>I</i> 230	SER A G C G 290	SER A G C ( 350	
	ASN SER	SER AGTA	SER P	
	ASIN A A T	LYS LYS A A A A A A A A A	ILE TYR TTTACT	
	ASN LYS ILE THR VAL ASN SER ASP ILE ASN ILE A T A A A A T C A C A G T T A A T A G C G A C A T C A A T A T C 210 220 240	A A C C C T C T A T A  260SER LYS ASN ASN LYS LYS SER SER VAL LYS ILEG C A A A A A C A A A A A A A A G T A G C G T T A A G A T T G C A A A A A C A A A A A A A A A A A A		
: :: :	ILE THR V.TCACAG'	A ASN ASN A A T A 280	 G THR J A C T A 340	: : :
ILE THR ALA LYS ATAACCGCCAAAA 200	ILE A T C	CTAACCCTCTATA 260SER LYS ASN ASN GCAAAACAA	SER THR THR ASN  TCTACCACTAACG 320 GLY ASN LEU THRGAAACTTAAC'	ASP ILE HIS LYS ASN ILE THR LEU ASN GATATCCATAAAACATTACGCTTAACA 370
ALA G C C A	LYS A A A A	LEU CTCT LYS AAAA	SER THR THR C T A C C A C T 7 320GLY ASNGA A A C T	LEU CTT?
THR ACCO	A T ? 210	A A C C C 260 SER 1 G C A 370	THR TACC 320 GLY GA	THR A C G C 380
	: : :	C T	SER T C	ILE ATTA 3
ASN THR PHE VAL ASN A A C A C C T T G T T A A C 190		LYS GLY GLY ALA HIS A A A G G T G G C G C C A C 250	ASN GLY ASN ILE THR AATGGCAATATTACT 310	ASIN A A C
3 VAL TGTTA 190		LYS GLY GLY ALA HIS A A G G T G G C C C A C 250	N ILE T A T T A 310	LYS A A A A A A A A A A A A A A A A A A A
ASN THR PHE ACACCTTT 190		GLY GGC	ASN GLY ASN ATGGCAATA 310	ASP ILE HIS ATATCCAT? 370
班 ACC		GLY GGT	G G C	ILE A T C
ASN A A C		LYS A A A	ASN A A T	ASP G A T

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	139/235		
SER T C T 420	LYS A A A 480	LEU CTA 540	TRP T G G 600
G G T	ILE A T C	SER T C C (	SER T C T
G G G	VAL GTA	VAL G T C	ASN A A C
ALA G C T (	SER T C T C 470	ASN A A C 530	SER A G C <i>1</i> 590
ILE THR TTACCO	GLU GAAT	ASN A A T 7	SER AGIP
ILE A T T	SER T C A G	PHE TTT?	ILE
THR GLY TYR LEU ASN ILE THR ALA GLY GLY SER CAGGTTACCTGAATATTACCGCTGGGGTTCT 390 400 420	CGGAAATGAGA  CGGAAATGAGA  440 IXS GLY ARG GIN VAL SER GLU SER VAL ILE LYS AAGGCCCAAGTATCAGAATCTGTAATCAAA A450  450	CTCAGGTGTAG  CTCAGGTGTAG  500 GLY GLU GLY PHE ARG PHE ASN ASN VAL SER LEU GGGAAGGCTTTAGGTTTAATAACGTCTCCCTA  520  520	ACTGCGCTTCG  560VAL GLY GLN LYS ASN ILE SER SER ASN SER TRPTGGTCAGAAAATATCAGTAGCAACTCTTGGT7GGTCAGAAAATATCAGTAGCAACTCTTGG
LEU CTG	 3 A GIN C A A G	 G PHE T T T 55	 G LYS A A A A 580
TYR TACO	CGGAAATGAGA 440LYS GLY ARG GLNAGGGCGCCA	GLY VAL GGTGTAG GLU GLY PHE	ARG PHECGCTTCGLGCTCGCTTCGGLYGIN
G G T	ASN A A T GLY G G G	GLY GGT GLU GAA	ARG CGC GLY GGT
THR GLY CAGGT	LYS ALA GLY ASN A A G C C G G A A A T C 440LYS GLY A A G G C C	C T C A G G T 500GLY GLU G G G A A 510	'Y LEU 560VAL T T C
: : :			
	LYS A A A	VAL ILE THR STTATCAC(	ALA GLY GCAGG
	GLU G A G	VAL GTT O	VAL GLY 3 T T G G C G 550
	所臣 G T T C G 430	GLY VG G G A G 490	VAL (GTTG 550
	VAL ALA PHE GLU LYS ALA GTAGCCTTCGAGAAAGC 430	ALA GIN GLY VAL ILE THE GCCCAGGGAGTTATCAC 490	ASN GLY VAL GLY ALA GL) AATGGCGTTGGCGCAGG 550
	VAL G T A	ALA G C C	ASN A A T

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ARG A G A (

ASN A A T 660	TRP T G G 720	SER A G T 780	
VAL G T A	TYR T A C	ALA G C C	
LYS A A G	ARG THR TYR GCACCTACT	ASP 3 A C	
GLY G G A 7 650	ARG C G C J 710	SER ILE ASP ALA AGTATCGACGCCA 770	
SER LCA(	GLY 3 G G (	SER A G T A	
620 ASP GLY ASN LEU ASN ILE SER GLY LYS VAL ASN A T G G G A A T T T A A T A T C T C A G G A A G G T A A A T 630 660	CGGGACAAAGT  CGGGACAAAGT  680 TRP HIS THR ARG ILE ASN GLY ARG THR TYR TRP GGCATACAAGAATTAACGGGCGCACCTACTGG GGCATACAAGAATTAACGGGCGCCTACTGG 690	CGTTGCCTCAG  T40  CGT SER SER PHE ASN LEU SER ILE ASP ALA SER  CGT GACGCCAGT  780  770	
ASN A A T A	ILE ATTA	ASN A A T (	
 LEU A LTAA, 640	 T ARG 1	 3 PHE 7	· · · ·
ASP GLY ASN LEU A T G G G A A T T T A A	ER GLY THR LYS C C G G A C A A A G T 680TRP HIS THR ARG G G C A T A C A A G 690	SER TCA( SER	ASP 3 A C i
GLY 3 G G 7	SER GLY THR LYS I C G G G A C A A A ( 680TRP HIS THR G G C A T A C P	LEU ASN VAL ALA SER TAAACGTTGCCTC? 740GLY SER SERGTAGTAG1	ASN GIN ASP ASP AACCAGGACGAC 800
620 ASP A T (	C G G G P 680 TRP G G C	C G T T 740 GLY G T 750	GIN C A G ( 800
: : :	<b>遠</b> ひ	ASN A A C (	ASN A A C
	VAL G T A I	LEUCTA	SER GLY
0	ASP G A T G O	THR ACTC	SER TCA(
610	SER MET A CAATGG 670	THR ACCA 730	SER S TCTT 790
	SER T C A	ASN VAL THR ATGTAACCA 730	GLY ILE GAATTI
	VAL SER MET ASP VAL S GTTTCAATGGATGTAT 670	ASN VAL THR LEU ASN VAL ALA SER A A T G T A A C C T C T A A A C G T T G C C T C A G 740GLY SER SER PHEGLY SER G T T G	GLY ILE SER SER GLY ASN GLN ASP ASP GGAATTTCTCAGGTAACCAGGACGACA 790

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PHE T T T 840	THR A C G 900	VAL GTT 960	SER
THR ACAT	LYS A A A A	SER T C A	THR
ILE A T A A	ILE A T C <i>I</i>	ILE A T T 1	班
ASN GLY A A T G G C P 830	HIS CATA 890	ASN A A T A 950	HIS
ASN A A T (	PHE LTT(	GLY 3 G A 7	THR
LEU . PTAA	ASN AACT	ASN GLY AATGGA	SER
GLY 5 G T 7	ALA 5 C T 7	РНЕ : Т Т ?	SER
ARG (	  THR A C A G	  LEU F F T A T	· · · · · · · · · · · · · · · · · · ·
THR ASN ARG GLY CAAATAGGGGTT 820	ALA 3 C A C SER '	SER TCGA ALA GCAT	GLU 3 A A C ALA
THR ACAA	ASN ILE A A T A T C C 860 GIN GLY A G G G C T 870	ASN AACT TYR I	PHE L T T C ASN
ILE THR ASN ARG GLY LEU ASN GLY ILE THR PHE TAACAAATAGGGGTTTAAATGGCATAACATT 810 820 830	ASN 1 A T 7 160 160 GIN A G (	AS PRO ASN SER  A C C C A A C T C G A  920  ASN TYR ALA LEU PHE ASN GLY ASN ILE SER VAL  A C T A C G C A T T A T T T A A T G G A A T A T T T C A G T T  940  960	ASN A C 3 80 LEU
		ZYS A	VAL 3 T C A 9
	THR ACT	PRO	THR ACTO
	ASN A O A	THR A C C (	GLY THR SGAACT )
	GLU 73 A A A 8 850	VAL MET THR STAATGACCC 910	GLY GLY G SGAGGAG 970
	ASN GLY GLU . A T G G A G A A 85	VAL 3 T A 7	GLY 3 G A (
	ASN GLY GLU ASN THR ] A A T G G A G A A A A A C A C T T 850	SER VAL MET THR PRO I TCAGTAATGACCCCTA 910	LEU GLY GLY GLY THR V TTAGGAGGAACTG 970

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LYS	1080		THR 1 C T 1140	1/1/1	T T 1200	•
ASN LEU	⋖1.		LEU ILE LYS ASN ASN LEU THR LEU ASN ALA THRTAATAAAATAATTTAACTTTAAACGCTACT1110 1120 1140	∑ T ∨ 1.		
ASN	AAT (		THR LEU ASN ALA CTTTAAACGCTA 1130	ARG TIE GIM IVS CIV	A A A O	
LYS LEU	A T T A 1070		LEU TTTA 1130	N	T C A A . 1190	
LYS	A A A		THR ACT 1	[±	ATT 1	
SER	T C A		ASN LEU AATTTAA )	DRG	2 0 0	
GLY	G G G		ASN A A T	S. C.	T C G	
T C A A A A T T T A  1040ASN VAL SER GLY	G G T G 1060	: : :	LEU ILE LYS ASN AS TAATAAAAATAA 1110 1120		GATT 1180	: ::
PHE T T T SER	TCA	PHETTT	LYS A A A	VAL G T T	A C C	GLU GAA
SER GIN ASN PHE TCTCAAAATTTTA 1040ASN VAL SER GLY	C T C	ASN THR ALA PHE A A T A C C G C T T T T T 1100	ILE A T A	ILE LYS GIN VAL A T T A A A C A G G T T G 1160	GGT	ILE ILE PHE GLU ATAATTTTGAAG 1220
T C A A 1040	A T	N THR TACC 1100	IEU T A 1110	E LYS T A A A 1160	A G	JE ILE LA A T T 1220
SER T C	•	ASN A A T	: : :	ILE ATT 1	: : :	ILE A T A 1
GLY ALA ILE ILE ASN GGCGCAATTATAAAT 1030		SER THR		GLU GAA		
E ILE FTATA 1030		SER TCA 90		ASN ILE ATATAG 1150		GIN C A A
ALA ILE ILE CAATTATA? 1030		ALA SER GLY SER THR GCTTCAGGCTCAACA 1090				VAL ALA GLU GIN ASN GTAGCCGAACAAAC 1210
ALA G C A		ALA SER		GLY G G T 7		ALA G C C
G G C G		ALA G C T		GLY GGAG		VAL G T A

143/23	5
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GLY GLY ASN ILE THR LEU GLY SER GLN LYS ALAGGGGTAACATCACCTTGGCTCCCAAAAGCC1230 1240	PRO THR GLU ILE LYS GLY ASP VAL THR  CCAACAGAATGTTACCG  1270 VAL LYS GIN GLY THR ASN ALA THR LEU ARG SER TCAAACAAGGAACCAACGCACTCTCAGAAGC  1320	ALA ASN PHE ASP ASN HIS LYS GLY ALA  G C G A A T T T T G A C A A C C A C A A G G T G C C T  1330 LEU ILE VAL ASN GLY ASN VAL THR ALA ASN GLY TA A T T G T G A A T G G A A A C G T T A C C G C C A A T G G C 1350  1380	ASN LEU THR ALA ASP GLY ASP THR ILE A A C C T T A C T G C G G C G A C A C T A T T A  1390 LYS ILE LYS GLY ASN LEU ASP VAL ALA GLN GLY  A A A T A A A G G C A A T C T T G A T G T T G C A C A A G G C  1440
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ASIN GLY GIN LYS ASIN

AAT GGGAATTTA CAA AACAAA ⊱ Ø ILE

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GLU GAA 1680	ASN A A T 1740	THR A C A 1800	ASN A A C 1860
ILE A T T	VAL G T C A	SER A G C	LEU
ALA GLU GCTGAAA	LYS A A A G	SER I C A A	ASN A A T C
N ALA NTGCT 1670	ASP F G A T A 1730	SER PAGTT 1790	ASP A G A C A 1850
ASN A A T (	SER 7	SER PCTA 17	THR ACAG 18
ASN ASN SER ASN A A T A A T A G T A A T C 1660	SER .	SER S	PHE T C A
ASN A A T A	ILE ATTT	GLU 5 A G 7 0	THR
	G C A A A A G A A G  G C A A A A A G A A G  1700 GLY ASN LEU THR ILE SER SER ASP LYS VAL ASN GTA A T C T C A C A T T T C T G A T A A G T C A A T  1740  1740	R ILE LYS ALA A A T C A A G C A G 1760GLY VAL ASP GLY GLU SER SER SER THRGC G T G G G G G G G T C T A G T C C A G C A C A 1780 11700 11700 1180	A A 840
ILE THR ASP TTACGGACA1650	G C A A A A G A A G  G C A A A A A G A A G  1700 GLY ASN LEU THR  G T A A T C T C A C	R ILE LYS ALA A A T C A A A G C A G 1760 GLY VAL ASP GLY G C G T T G A T G G (	LYS A A A i GLU 3 A G 1
THR A C G (	GIN LYS GLU C A A A A A G A A 1700 CGLY ASN LEU GLY ASN LEU GT A A T C T G	ILE THR ILE LYS TAACAATCAAAG 1760GLY VALGCGTTG	ILE ATTA LYS AAA(
ILE T T 7	R GIN 1700 GLY G T 7	A A T C . 1760 GLY G C (	U THR ILE A A C C A T T 1820 THR LYS C C A A A 0
: : :		THR ACAA	LEU CTAZ 12
	ILE SERATCTCO	ILE A T A	ASN A A T (
	ASN A A T	THR LYS GIN CCAAACAGA 1750	ALA G C C Z
	GLY A 3 G C A 1690	LYS A A A (	ASP PS AT G
	LE GLY GLY ASN ILE SE TTGGCGCAATATCTC 1690	LE THR LYS GIN ILE TH TTACCAAACAGATAAC 1750	LA SER ASP ALA ASN LEU THR ILE LYS  CAAGTGATGCCAATCTAACCATTAAAA  1810 THR LYS GLU LEU CCAAAGAGTT.
	T T (	TTA A	ALA C A i

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ASP LEU ILE ILE GLY	GATTTAATTGGC 1910 1920		LYS VAL LYS ASP SER A A G G T T A A A G A T T C A	1970 1980		GLU THR SER ASN SER	GAAACGTCTAATAGC	2030 2040
ILE SER GLY PHE ASN LYS ALA GLU ILE A T T T C A G G T T T T A A T A A G C A G A A T T A  1870 THR ALA LYS ASP ASN SER ASP LEU ILE ILE GLY	CAGCTAAA18901890	CTAGCAGTGACAA 1930	LYS GLN VAL TF		LYS ILE SER ALA GLY ASN HIS ASN VAL A A A A T C T C A G C T G G C A A T C A C A T G T A A	1990 2000 THR LEU ASN SER LYS VAL GLU THR SER ASN	CACTAAATAGCAAAGTGGAAACGTAATAGC	2010 2020

AGCGAT AACGGT GGA 'AGCACCG 2050 閨 SER CGT GAT ASP

1 G T A 'A G T C 2270

SE

VAL

	147/235		
LYS A A A 2100	TAATATCACCT  2120SER HIS LYS THR VAL ASN ILE SER ALA SER GLUCTCACAAAACAGTAAATATCTCTGCATCAGAA2130 2140 2160	VAL G T A 2220	
ALA G C A	SER T C A	GLU GAA	
SER T C C	ALA G C A	VAL G T G	
ILE LATT 2090	SER 7 T C T 2150	SER 7 A G C 2210	
THR ACT 2	ILE ATC 2	GLY GGT 2	
LEU T T A	ASN A A T	THR A C A	
ASP ASN ILE GLY LEU THR ILE SER ALA LYS ACAACAATATCGGCTTAACTATTCCGCAAAA 2070 2080 2100	TAATATCACCT  2120SER HIS LYS THR VAL ASN ILE SER ALA SERCTCACAAAACAGTAAATATCTCTGCATCAG2130 2140 2150	A G C A G G C A C A A  2180  THR ILE ASN ALA THR THR GLY SER VAL GLU VAL C C A T T A A T G C G A C C A C G G T A G C T G G A A G T A 2220	
ILE G ATCG 2080	 T THR VA A C A G '	 ALA TI GCGA(	
ASN A A T	TAATATCACCT 2120 SER HIS LYS THR CTCACAAAAC	A G C A G C A C A A 2180THR ILE ASN ALACCATTAATGC 22390	TATTAGCGGTA
ASIN A A C	ILE A T C HIS C A C	ALA GLY THR GCACACA 180 THR ILE ASN CCATTAAT 2190	ILE SER GLY ATTAGCGG1
ASP A C	T A A T 2120 SER C T C T	S ALA A G C A 2180 THR C C	ILE A T T
	ASN A A T	THR ACTA	GLY GGC(
	IR VAL 2 G G T A A 2110	E THR CACTA 2170	THR ACA(
	THR A C G 21	11.E A T C P 2170	LYS A A A A
	ASP VAL THR VAL ASN SETGATGTA A TAG	GLY GLY ILE THR THR LYSGGAGGTATCACTACTAA 2170	THR ALA LYS THR GLY ASI ACTGCTAAAACAGGCGA
	ASP G A T	GLY GGAA	THRACTO

SER THR GLY ASP LEU THR VAL ARG LYS A G C A C T G G C G A T T T A A C T G T T A G G A A A G 2290ALA ALA THR ILE SER VAL THR GLU GLY ALA ALAC T G C A A C C A T T A G T G A G G A G C T G C A	THR LEU THR ALA THR GLY ASN THR LEU  A C C T T A A C C G C A A C A G G A A T A C C T T G A  2350  THR THR GLU ALA GLY SER SER ILE THR SER THR  C T A C T G A A G C C G G T C T C A C T C A C T  2380  2340  2400	LYS GLY GLN VAL ASP LEU SER ALA GIN  A A G G G T C A G C T T T C A G C T C A G G  2420 ASP GLY SER ILE ALA GLY GLN ILE SER ALA ALA ASP GLY SER ILE ALA GLY GLN ILE SER ALA ALA  2460  2460	ASN VAL THR LEU ASN THR GLY THR A A T G T G A C A T A A A A A G G C A C C T 2470
SER TAGCA	THR L	LYS G AAGG	ASN VA

SER T C G 2700

ATC

A A A 2 K

G G G

TAAAT

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... TAAGCACA

EEG. : 2660

ASIN

PEI

ASIN

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CACCGGG

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TCA

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	149/235		
ALA G C A 2520	GLY G G T 2580	THR A C C 2640	
LYS A A G	SER T C A	LYS A A A	
ILE A T T	ALA G C A	ALA G C G	
ASN A A C . 2510	THR TACG 2570	GACT (2630	
SER I C A 1	GLY 3 G T	VAL 3 T G Z	
GLY 3 G T	ASP 3 A T (	SER AGC	
GLU GAA(	LEU CTA(	GLY G G T A	
VAL G T A G 2500	  LYS LI A A G C 7	 G SER GI T C T G (	:
LEU THR THR VAL GLU GLY SER ASN ILE LYS ALATAACTACTGTAGAAGGTTCAAACATTAAGGCA2490 2500 2520	THR SER GLY THR LEU ALA ILE ASN ALA ACCAGTGCCACTTAGCTATTAACGCAA 2530LYS ASP ALA LYS LEU ASP GLY THR ALA SER GLYAAGACGCTAAGCTAGATGGTACGCATCAGGTAAGACGCTAAGCTAGATGGTACGCATCAGGT2550	ASN ARG THR GLU VAL ASN ALA THR ASN A A C C G T A C A B A G T A A T G C A A C T A A G G  2590 ALA SER GLY SER VAL THR ALA LYS THR C A A G T G G T T C T G G T A G C G C A A A A C C  2640	ASP
THRACT	ASN A A C ASP G A C	THR ACT SER AGT	GLY
TAA	A ILE T A T T 2540LYS A A A A	N ALA T G C A 2600 ALA C A	THR GLY
: : :	ALA G C T 2 2	ASN A A T 2	ILE
	LEU TTA	VAL G T A	ASIN
	THR A C C	GLU GAA 90	VAL
	GLY 1 G G C A 2530	THR (A C A G 2590	ASN
	SER A G T	ARG C G T	SER
	THR ACC	ASN A A C	SER

### **IG.25N**

GLU ASN GLY ARG ASA CACTGTG CGTTAA  GAAAATGGTAGAACACTGTG CGCTTAA  2720ARG GLY LYS GLU ILE ASP VAL LYS TYR ILE GLNCAG GCAAGGAAATTGATGATATATCCAAS2730  PRO GLY VAL ALA SER VAL GLU GLU VAL  CCAG GTGTAGCAAGAGAGAGAGAA  2740  2740  2750  2760  ASP VAL LYS TYR ILE GLN 2760  2760  2760  RO GLY VAL ALA SER VAL GLU GLU VAL  CCAG GTTAGCAAGAGAGAGAGAGAA  2770  2770  2780  ASP IEU SER ASP GLU GLU ARA GCGAAACGCGTCTTGAGAAAAAAAAAAAAAAAAAAAAA
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SER T C A 2940	VAL G T A 3000	
PRO C C G	ALA G C A	
ASN THR GIN ASN GLU PHE THR THR ARG PRO SER ATACACAAAATGAATTTACAACCAGACCGTCA 2910 2920 2940	GLU GLY LYS GAAGGTAAGG 2960ALA CYS PHE SER GLY ASN GLY ALA ALA VALCGTGTTTCTCAAGTGGTAATGGCGCAGCAGTACGTGTTTCTCAAGTGGTAATGGCGCAGTACGTGTTTCTCAAGTGGTAATGGCGCAGTA	
THR A A C C 2930	GLY F G G C 2990	
THR ACA	ASN AAT	
PHE T T T	GLY GGT	
N GLU TGAA 2920	SER AGT	
ASN A A T 29;	 G SER S T C A A 2980	: ;: :
GLN C A A	SER GIN VAL II.E II.E SER GLU GLY LYS A G T C A A G T A A T T T C T G A A G G T A A G G 2950 2950 2950 2950 2950 2950 2950 2970	CYS THR ASN VAL ALA ASP ASP GLY GIN GTACCAATGTTGCTGACGATGGACAGC 3010 3020 ***PRO ***
THR A C A	GLY GGT CYS TGT	ASP GLY 1 G A T G G A 3020 PRO *** C G T A G 3030
A T	GLU F G A A 2960 ALA C G	ASP GLY 3020PRO *** C G T A G3030
	SER TCT	ASP G A C
	SER GIN VAL ILE ILE GTCAAGTGATAATTT 2950	CYS THR ASN VAL ALA ASPGTACTGAC GTACCAATGTTGCTGAC 3010
	L ILE GATA 2950	N VAL 1 T G T T 3010
	VAL A G T G 29	ASN 3C A A T
	GIN FCAP	THR
	SER	CYS

FIG.26/

Strain 15 hmw1A sequence	LYS GLU TRP LEU LEU ASP PRO ASP ASN VAL A A A G A G T G T T A G A C C C G G A T A A T G T A A  30  10 THR ILE GLU ALA PRO SER TYR SER ARG GLYCAATTGAAGCCCCTTCCTATTCTCGCGGT	ASN ALA GLY ILE ASP SER GLU PHE PRO GLY A A T G C C G G T A T A G A T A G T G A A T T C C C G G C C  90 70 80GLY SER GLY THR LYS GLU SER PRO LYS THRGT T C G G C A C A A G G A A A G C C C T A A A A C A A C C C T A A A A C A A G C C C T A A A A C A A A G C C C T A A A A C A A A G C C C T A A A A C A A C A A G C C C T A A A C A A C A A G C C C T A A A C	ASN GLY GLU GLN PRO THR VAL LEU THR ASN A A C G G C G A C A G T A T T A A C C A A T G  130 GLU THR ILE SER ASN TYR LEU LYS SER GLY A A A C C A T T T C A A A T T A T C T G A A A G C G G C 180
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SUBSTITUTE SHEET (RULE 26)

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ILE A T A 420	ALA G C G 480	ILE A T T 540	PHE
SER T C C A	THRACCG	SER	ARG A G A T
THR LEU ASN ILE THR ALA LYS GLY SER ILE CCTTGAATATTACAGCTAAAGGATCCATA 400 420	THR GLU LYS ALA  TACAGAAAAGCCC  440 ARG ASN ALA SER SER ALA GLN ILE THR ALAGCAACGCATCAAGCGCTCAAATCACGGCG 480	ASP GIN GATCAAA 510 LEU ARG LEU ASN ASN VAL SER ILE CTCAGACTTAATAATGTATCTATT 520 530	LEU ASN PHE VAL T T T A A A T T T G T T T 560 570 SER ILE GIN PRO ASN THR SER HIS ARG PHE C A A T T C A C A C A C A C A C A C A C
LYS A A A 410	GEN C A A A 470	ASN A A T 530	SER T C T C
ALA G C T A 4	ALA G C T	ASN A A T I	THR ACTT
THR ACAG	 C SER A G C (	 A LEU C T T	T T 0 ASN
ILE AATTA	ALA G C C 450 SER T C A	GIN C A A 510 ARG A G A	VAL FGTTT 570 PRO
ASN J AATA 400	CGGTACAGAAAAGCCC 440 4.3 ARG ASN ALA SER SERGCAACGCATCAAG	CAATACTGGCGATCAAA 500 510LYS GIN LEU ARG LEU 520 520	AGGTTTAAATTTTGTTT 560 570 SER ILE GIN PRO ASN CAATTCAGCCTAA
LEU TTG	GLU G A A ASN A A C	GLY GGC GIN CAA	ASN A A T ILE A T T
THR LEU	THR A C A 440 .ARG . G C	THR TACT 500 LYS AA	GLY LEU ASN GGTTTAAATT 560SER ILE
: : :	G G T	ASN A A T 	G G
	J GLY G G G A 430	ILE A T A A 90	GLY G G T
	GLU G A G (	THR ] ACTA 490	THR (A C G G S S S S S S S S S S S S S S S S S
) }	ALA PHE GLU GLY ASI GCCTTTGAGGGAAA 430	GIN GLY THR ILE THE CAGGGAACTATAAC 490	ASN GLY THR GLY ILA AATGGGACGGGTAT 550
5	AIA G C C I	GIN C A G G	ASN AATG

ASP GLY GLU LEU ILE ILE SER GLY ARG VAL  GATGGGAGTAC  620  630 HIS VAL ASN GLN THR THR PRO LYS ASN LEUATGTTAATCAAACCTAAAAACCTGATGTTAATCAAACCTAAAAACCTG	SER PHE TRP LYS VAL SER ASP GLU SER TYR  TCTTTTTGGAAGGTATCCGATGAATCTTATT 670 680 670TRP ASN VAL SER HIS LEU THR VAL LYS GLUGGAATGTCAGCCATCTTACCGTAAAAGAG 720	LYS SER ALA PHE SER PHE THR LYS PHE ALA  A G T T T G C G T  750  730 LEU ASN ASN ASN HIS GLY ARG GLU THR SER TAAATAACAATCATGGCCGAGAGACTTCC 780	ARG TYR ARG LYS GLY GLY VAL ILE PHE A G A T A C C G C A A A G G T G G G G T G T A A T C T T T C 790 800 810
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107.DI	ARG SER PRO THR GLY HIS THR ASN PHE THR G C T C A C C G G T C A C A A A T T C A C A 830 840
VAL LYS GIN GLY SER G T T A A A C A A G G C T C A 850	SER VAL ALA ASN PHE SER CAGTGGCTAATTTTCAT 860 870 PHE LYS ALA LYS ASN ASP THR ASN HIS ALATCAAGGCAAAAATGATACAAATGCA 890 900
ASN GIN LEU PRO ] AATCAACTCCGA 910	ASN GIN LEU PRO ILE GIN PHE ASN SER ASN A A T C A A C T C C G A T T C A G T T T A A C T C T A A T A 910IIE SER VAL ASP GLY GLY GLY LYS VAL LEUT C T C A G T C G A T G G A A A G T C C T T 940 950
PHE CYS ILE THR SER TTTTGTATAACCTC()	SER ASN TYR SER GLY ARG CCAACTACTCCGGCAGAT 980 990 SER VAL GLY ILE GLY MET SER SER ILE ASN CAGTGGGATAGGAATGTCTAGCATTAAT 1020

# FIG.26F

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VAL SER ASP GLY SER ASN LEU THR PHE ASN G T T C T G A T C C T T A C T T T T A A T T 1030 1030SER SER ILE ARG GLY GIN GLU ALA PHE ASNC T T C C A T T C G C G C C A G G A A G C C T T T A A T 1080	ILE SER LYS ASP LEU THR ILE ASN ALA THR A T C A G T A A A G A T T T A A C C A T A A A T G C A A C C G 1090GLY SER PHE PHE GLU LEU GLY GLN TYR SERGTTCATTTTGAACTTGGGCAATACTCG	ASP THR PHE ASN GLY PHE ASN HIS  GATACCTTTAATGGTAATGGCTTTTAACCACG  1150 ASP ALA ILE LYS SER THR HIS ASN ILE SERACGCCATTAAATCAACTCACAATATACO 1200	ILE LEU GLY ALN VAL THR LEU GLY GLY ATCTTAGGTGGCAATGTTACCCTTGGCGGGC

FIG.26G
A A G A T T C A A G C A G T A C C A T T A C A G T A A T 1240 1250 1260
ILE ASN ILE SER GIN ALA ALA ASN VAL THR A T C A A T C T C A G C A G C A A T G T T A C C T 1280 1270LEU ARG ALA TYR ASN GLY ASN GLY ARG ASNT G C G A G C T T A T A A T G G T C G A A A C 1320
LYS GIN LEU THR LEU GLY ASN VAL SER ILE A A A C A A C T A A C C A A T G T A T C T A T T G 1330 1340 1350GLU GLY ASN LEU SER LEU ILE GLY ALA SERA A G G G A A T T T A A G T T T A A T C G G T G C A A G T 1380
ALA ASN ILE ASN GLY ASN LEU SER VAL LYS GCAAATATTAACGGCAACCTTTCCGTTAAAG 1390 1400 1400 1410GLU ASN ALA LYS PHE LYS GLY GLU THR GINAAAATGCTAAATTTAAAGGGGAAACCCAA

# FIG.26H

ASP ASN LEU ASN ILE THR GLY THR PHE ILE G A C A C C T C C G C C C C T T T A T C A 1450 1ASN ASN GLY ASP SER LYS ILE ASN ILE SERAT A A C G C C G C C C T T T A A A T C A T A T A T C T 1480 1500	GIN GLY VAL VAL LYS LEU GLY ASN VAL THR  C A A G G A G T G G T A A A C T T G G C A A T G T T A C C A  1520  1520 ASN ASP GLY ASP LEU ASN ILE THR THR HIS  A T G A T G G T G A T T T A A A C A T T A C C A C T C A C  1560	ALA LYS HIS ASN GIN ARG SER ILE ILE GLY GCTAAACACCAAGCATCATCGGCG 1590 1570GLY ASP ILE ILE ASN LYS GLY SER LEUGLY ASP ILE TAATCAACAAAAGGAAGCTTAGAGATATAATCAACAAAAAGGAAGCTTAGAGATATAATCAACAAAAAGGAAGCTTAGAGATATAATCAACAAAAAAGGAAGCTTA	ASN ILE THR ASP SER ASN LYS ASN ALA GLU A A T A T A C A G A C A G T A A T A A G A A T G C T G A A A
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AAA AAA 1680 CAA ACC ATC GLN 開 CTA ATATCTCG ... TCAATATTACCAATCAGATAACA LEI SE 强 GCCAAT ASN 1730 SEN ASIN ALA Ø AAT  $\mathcal{C}$ ASN ASIN GLY GAGAATTCCGATTCAG... <u>ი</u> ATTTCTTCCGATAAA... 1710 ... TCCAAATTGGC ... ACGCGACAAAC 闺 ASIN GLY 1660 ASP ASP 田田田 ASN ALA GLN ...ASP ...ILE ASIN GEU ACG 999 開 GLY AATCTC GTTGAT ASP 日日 ASIN G G C GGT GAA GCA

ALA ် ဗ TTTCAGGTTTCAATAAA ASIN 盟 GLY GACC... 1830 段 CAAGIN Ø TTGAAATTAACG ASIN AA Ø EI. E E 1820 LYS 图图 AAAGAA 1810 LYS

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0 0 C AGTACT GACCAT GAC 贸 000 GAT GGA ASP GLY GLY ... TTGGTAACACCAATAGTGCT ... AAGATTCAAAAATCTCTGCT GACAACACT ALA 開 ASIN SER ASN ASP AATGCCAAAAAGTAACCTTTAACCAGGTTA... ACTA... AATGTGACACTAAATAGCAAAGTGGAAACAT... 1890 ... CTGGTAATACT 出 CITO TTA GEN ASIN EEG A C A G C T A A A A A A T G G T A G T G A T ASP ASIN WAL 選 GLY ..LYS · · · ILE SER. 出 LYS 国 SE 開 段 GLY GLY WAL ASP ASIN LYS LYS 园 ASIN 1870 ALA ASIN 出 温 Ľ ILE ASIN Ø

FIG.26KAIA LYS ASN VAL GLU VAL LYS ASN ASN ILECGAAAATGTAGAAGTAAAAACAACATT 2080 2090 2100
THR SER ASN LYS THR VAL ASN ILE THR ALA ACTTCTAACAAACAGTAAATATCACCGCGT 2130 2110SER GLU LYS LEU THR LYS ALA ASP ALACAGAAAACTTACCACCAAAGCGGATGCA 2160
THR ILE ASN ALA THR GLY ASN VAL GLU ACCATTAATGCAACCACTGGTAACGTAGAAG 2170 2180 2190VAL THR ALA LYS THR GLY ASP ILE LYS GLYTGACAGCCAAAACAGGTGATATTAAAGGTTGACAGCCAAAACAGGTGATATTAAAGGT
GLU VAL LYS SER THR SER GLY ASN VAL ASN GAAGTCAAATCCACTTCCGGTAATGTAAATA 2250 2240ILE THR ALA ASN GLY ASP THR LEU ASN VALTTACAGCAAACGGCGACACGCTTAATGTA 2280

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GLN C A A 2340	SER A G T 2400	THR A C T 2460	
IR A C C	GLY 3 G C	THR 1 C T	
THR ACCA	ASP 3 A T (	LEU PTAP	
LEU TAA 30	LYS A A G G 390	THR J	
LYS LEU AATTAA 2330	ALA LYS CCAA 2390	GLY THE ; G C A C 2450	
A	A D	D 9	
 A GLY G G C	 C THR A C A G	 A THR	: : :
THR ILE A C C A T C A 2310 ASP LYS GLY S A T A A G G G C 2320	GLY GGCC 2370 LEU CTTA	VAL G T G 2430 THR A C C	SER A G T G 2490
THR A C C A ASP I 3 A T A 2320	ASN CARATG	ASN A T G ASN T A ASN T A A T A A T A Z440	ALA 3 C C /
ALA VAL THR GCTGTTACCA OO THR ALA ASP CTGCAGATA CTGCAGATA	SER ASN ASN GLY CAAACAATGG 60 237 GIN THR THR LEU AGACAACTCTT	ALA 5 C C 7 LEU T A P	ALA ; C A C
	TTACCTCAAACAATGGCC 2360 2370GIN THR LEU THR ALA LYS ASP GLY SER AGACAACTCTTACAGCCAAGGATGGCAGT	LE ASN AIA ASN VAL  TCAATGCGCCAATGTGA 2420 2.420THR LEU ASN THR THR GLY THR LEU THR THRCATTAAATACCACAGGCACTTTAACTACT 2460	ILE ASN ALA TTAACGCAG 2480
ASN 1 G 23 23 23	THR 23 23(	AT G 24	LE ASI TTAA 2480
GLY S G C A	ILE	ILE 7	C A I
	<b>H</b>	II	ASI A A
VAL SER TTTCA 2290	SER A G C 50	SER A G C.	SER ASN TCAAACA 0
VAL S G T T T 2290	SER S TCTA 2350	ALA GLY S C A G G A A 2410	GLY S G G T T 2470
ASN A A T G	SER A G C 1	ALA 3 C A	VAL GLU GLY TAGAAGGT 247
SER ASN VAL SER (A G T A A T G T T T C A G 2290	ALA SER SER SER GCAAGCTCTAGCA 2350	ILE ALA GLY SER ] A T C G C A G G A A G C A 2410	VAL GLU GLY SER ASN ILE ASN ALA ALA SER GTAGAAGGTTCAAACATTAACGCAGCCAGTG 2470 2480
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### FIG.26N

ALA G C G 2760	LYS A A A 2820	GLN C A A 2880
GLU G A A	ALA G C T	THR A C A
TATCCAGCCAGGTG  2720 VAL ALA SER VAL GLU GLU VAL ILE GLU ALA  2740  2750  2760 TAGCAAGTGTAGAAGTAATTGAAGCG	AGTGAAAGATTTAT 2780 SER ASP GLU GLU THR LEU ALA LYS CTGATGAAGAAAGAAACATTAGCTAAA 2820	ACGTTTTATTGAAC 2840 2850PRO ASN THR ILE THR VAL ASN THR GINCAAATAACCATTACGGTTAACACAA 2860
VAL A G T A 2750	THR A A C A 2810	C VAL G G T T 2870
GLU GAA	GLU GAA	THRACG
TATCCAGCCAGGTG 2720 2720 2730VAL ALA SER VAL GLU 2740	A T ARG	  ILE A T T
G G T 2730 VAL G T A 6	SP LEU A T T T A 2790 JU GLU A A G A A 2800	GLU G A A 2850 THR A C C
PRO GI C C A G ( 2' SER VI A G T G 1	ASP G A T GLU G A A 28°	ILE (A T T G A T T G A S T A A T A A T A A T A A T A A T A A A T A A A T A A A T A A A A T A A A A T A A A A T A A A A T A A A A T A A A A T A A A T A A A A T A A A A T A A A A T A A A A T A A A T A A A A T A A A A T A A A A T A A A A T A A A A T A A A A T A A A A T A A A A T A A A A T A A A A T A A A A T A A A A T A A A T A A A A T A A A A T A A A A T A
ATATATCCAGCCAGGTG 2720 2730VAL ALA SER VAL GLUTAGCAAGTGTAGA	GAAAGTGAAAGATTTAT GAAAGTGAAAGATTTAT 2780	TGTACGTTTTATTGAAC  TGTACGTTTTATTGAAC 2840 2850PRO ASN ASN THR ILECAAATAATACCAT?
ILE	VAL A G T G 2780 SER C T	ARG A C G T 2840 PRO
TYR T A T	LYS A A A A	VAL GTA
JU VAL 1 G G T G 2710	ARG VAL LEU GLU GCGTCCTTGA 2770	SER AGTG 30
TEGIU TTGAGC 2710	VAL GTC 27	VAL S G T A A 2830
<b>∼</b>	LYS ARG VAL LEU GLA AAACGCGTCCTTGA 2770	LEU GLY VAL SER ALA CTTGGTGTAAGTGC 2830
GLU GAAA	LYS A A A C	LEU CTT

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TGT A G 0 0 0 GTTGCTGACGATGGACAGCAG GGTAAG LYS GAB ASP AGTCAAG... 2910 ATTTCT ASP SE SEC TTTACAACCAGACCATCA GGTAATGGCGCAGCAGTA SE ... T G ... A T ...VAL ... ASIN ARG ALA 班 選 ASIN 2890 AATGAG GLU TCA ASN SER

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### -1G.27A

NTHi strain 15 hmw2A sequence

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GLY G G	09	THR A C 120		DET E	1. T. 180
ALA G C A		ASP GAT		LYS ILE	A T. A
ASP G A C		ALA G C T		LYS	5 A B
GLY G G A	50	) SER GAGT 110		GLU	D A C
ALA G C A G	ιC	GLU GAG 11		LEU	170 T70
SER HIS MET PRO  CCCATATGCCG  20  GLU ASN VAL TYR ILE ASN ALA GLY ASP ALA GLY GAGAATGTATATTAATGCAGGAGACGCAGG		80 GLU TYR THR GLY GLU SER ALA ASP THR GAATACACAGGAACAGGAGAGAGTGCTGATAC 90 100 100 120		THR LEU THR ASN SER THR LEU GLU	A C A C T A A C A A C T C A A C G C T T G A G A T A T T 150 150 160 180
ILE		THR ACA(		SER	L C A 7
  TYR I A T I	40	 GLY 3 G A 1	: : :	ASN	A A C 1
PRO C C G VAL T	GLU . G A A.	THR ACA	THR. ACA.	景,	A C A
SER HIS MET CCCATATGC 20 GLU ASN GAGAATG	30 LEU GLU ASN GLU TAGAAAACGAA	TYR TAC.	ASN THR LYS THR ACACAAAGACA 140		C T A
HIS C A T 20 GLU G A G	30 GLU G A A	SU GLU GAA 90	THR ACA 0	開	A C A 150
SER TCC 2	30 LEU GLU TTAGA?	80 GLU G A 7	ASN TFA A CACACACACACACACACACACACACACACACACAC	•	A C 150
GLY GGA	ASN A A T		ASN A A T		
SER T C G	THRACT		ASN A A C		
ASN SER ALA SER GLY A T T C G G C T T C G G G A 10	ARG SER ASP THR ASN GTAGTGACACTAAT	70	PRO LYS ARG ASN ASN CAAAACGAAACAAT 130		
SER T C G	SER A G T		LYS A A A		
ASN SER ALA SER GLY SER HIS MET PRO GAATTCGGCTTCGGGATCCCATATGCCG 10 20 GLU ASN VAL T GAGAATGTATA	ARG SER ASP THR ASN LEU GLU ASN GLU		PRO LYS ARG ASN ASN A TCCAAAACGAAACAATA 130		
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## FIG.27B

	1007 230		
ILE A T 240	VAL G T 300	GLY G G 360	
ASP GATA	C C C	SER AGCO	
SER AGT	SER A G T	SER ICTA	
ASN A A T A	ASN A A C D	TYR FAC'	
VAL A 3 T T A 230	LYS 7 A A A A 2 290	ILE 1 NTTT 350	
ARG VAL ASN SER AGAGTTAATAGTO 230	ASN . A T ?	THR ILE TYR ACCATTTACT 350	
ILE ATCA	LYS ASN LYS ASN SER GLY A A A A T A A A A A C A G T G G C C 290	LEU	
VAL ASN ILE THR G T T A A T A T C A C T  200 ALA ASN ASN GLU ILE ARG VAL ASN SER ASP ILE G C C A A C A A T C A G A G T T A A T A G A T A T 240 210 220	 SER AGCP 280	ILE THR SER THR ATCACTTCTACT 320 ALA ASN GLY ASN LEU THR ILE TYR SER GLY GCTAACGGAAACTTAACCATTTACTCTAGCGG 340 350	LYS ASN ILE THR A A A A A T A T T A C G 380
ILE A T C ? ASN A A C ?	LEU CTAP TRP	SER ICTI	ILE A T T A
ASN A A T 7 0 ALA 3 C C 7 210	ER HIS LEU THR CCCACCTAACC 260 LEU TRP SER CTCTGGAGC	THR ACT' 20 ALA GCT? 330	LYS ASN ILE A A A A A T A T T 380
VAL ASN 3 T T A A 2 200 ALA G C 0	SER HIS T C C C A C 260 LEU C T C	ILE THR A T C A C T 320 ALA G C T	LYS A A A A A 380
SER T C T	GLY GGCA	GLY G G C A	ILE ATTO
GLY G G C 7 190	GLY G G A C 250	ASN A A T G 310	ASP G A T A 370
ARG A G A G	ILE A T C G	ILE A T T A	VAL GTTC
ALA ARG GLY SER PHE AGCAAGAGGCTCTTTT 190	ASN ILE GLY GLY ASN CAATATCGGAGGCAAC 250	LEU ILE ASN GLY ASN TCTGATTAATGGCAAT 310	TRP VAL ASP ILE HIS A T G G G T T G A T A T T C A T 370

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4 <del>4</del> <del>8</del>	THR A C 540	PHE T T 600
THR	GLY 3 G G	TYR
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Y G T C 1 470	1 GI TG(	VAL TEST CA C 590
GL) A G G	AST A A A	VAI G T
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ILE A T T	SER ICT	SER A G T C
·····································	. T. C. 520	ASN ATA
GLY G G T A P	ARG G A ASN A T G	SER ARG PRO CAGTAGACCA 560 GIN LYS ASN SER LEU VAL THR ASN TYR PHI . CAAAAAACAATAGTCTCGTCACAAACTATTT . CAAAAAACAATAGTCTCGTCACAAACTATTT . 570 570
A A G	HE TTA TTA I	ARG I
L A A A T A A T A A T A A T A A T	T C T G T G T G T G T G T G T G T G T G	SER A G T A G I A G IIN LY C A A A A G T A A A A G T A A A A G T A A A A
T 4 · · ·	A 10	7 ) IÔ
PHE T T T	LYS A A A	
ALA G C C	ASN A A T	ASN A A T (
VAL 3 T C	ASN A T	PHE T T T
ASP A T (430	GLY G C 7 490	GLY LEU LEU PHE ASN LEUTGCTTTTTAATCT 550
CY GAG	LA C A G	LEU ]
U G	R A G	GLY LI
GI A G A	T A C	GE.
	GLU GLY ASP VAL ALA PHE GLU LYS GLY AGAAGGAGATGTCGCCTTTGAAAAGGG 450 ASN ASN LEU THR ILE THR GLY GLN GLY THR ILE AATAACCTAACCATTACAGGTCAAGGAACTAT AATAACCTAACCATTACAGGTCAAGGAACTAT 450	GLU LYS GLY  T G A A A A G G G  ASN ASN LEU THR ILE THR GLY GIN GLY THR ASN 450  GLY PHE ARG  A G G C T T T A G A  A G G C T T T A G A  SOO  THR IEU ASN GLY THR GLY  A G G T C T C T C T C T C T C G G A C T G G A C T A C C A T T A C A G G T C A A G G A A C T A C C A T T C A A A A T G T C T C T C T C T A A A T G G C A C T G G G A C T G A C A C T G A A A A T G T C T C T C T A A A T G G C A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G C T G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G A C T G G G C T G G C T G G C T

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	開			ALA G C 720		PRO C C 780	
	ALA	G C T		ILE THR HIS LEU ASN TAACCCACTTAAATO		ASP GLY SER ALA SATGGCTCAGCCO 770	
	PRO PRO ASIN	AAT		LEU T T A		SER T C A	
	PRO	A C C T 650		c C A C 710		GLY GGC 70	
	PRO	C C A 65		THR ACC 71		ASP ( G A T G 770	
	ILE	ATT		ILE A T A		GLU GAG	
	MET	A T G		ASN A A T A		ALA G C A	
	620 VAL ASN ILE SER	GTAAATATCTCAATGATTCCACCTAATGCTAC 630 640	: : :	ARG THR TYR TRP ASN ILE THR HIS LEU ASN ALA CGAACCTATTGGAATATAACCCACTTAAATGC 690 700 700 720	: : :	ILE ASP SER SER ALA GLU ASP GLY SER ALA PRO A T T G A C T C G G C A G A G G A T G G C T C A G C C C C 750 750 760	
SBA AGC	HE	ATC	GLY GGGG	TYR T A T	THR ACT	SER T C C	G G C
GLY GGA	ASIN	AAT	LYS A A A	THR ACC	LEU CTT	ASP G A C	ASN A A C
ILE SER GLY SER ATTTCAGGAAGC	620 VAL	G T A	ARG TYR LYS GLY A G A T A C A A A G G G 680	ARG C G A 690	PHE ASN LEU THR TTTAACCTTACT 740	ILE A T T 750	THR LEU ASN GLY ACCTTAAACGGC
		: :	A.	: : :	PHE TTT 7		班 A C C 8(
ASN A A T			SER A G C		ASN A A C		TYR T A T
LEU TTAP			TYR TACI		SER AGCA		SER AGTT
THR ACT1	610		TRP T G G 1 670		ASP GATA 730		SER T C C A 790
ASN GLY ATGGGP	) )		SER ASN GCAATI		SER GLU CCGAAG		LEU TTAT
ASN GLY THR LEU ASN TAATGGGACTTTAAAT			SER ASN TRP TYR SER AAGCAATTGGTACAGC 670		SER GLU ASP SER ASN CTCCGAAGATAGCAAC		LEU LEU SER SER TYR TCTTTTATCCAGTTAT 790

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ILE SER PHE THR THR ASP THR THR PHE ASN VAL A T A T C A C C A C A C A C A C C T T T A A T G T 820 830 840	ASN LYS ASN ALA LYS VAL ASN PHE ASN  TAATAAAAATGCAAAAGTCAACTTTAAC  850  ILE LYS ALA PRO ILE GLY THR ILE ASN GLN TYR 75  ATCAAAGCACCAATAGGGACTATAAATCAATA 900  800	ASN ASN LEU ASN TYR ALA LEU PHE ASN CAATAACCTGAATTACGCATTATCAAT 910 GLY ASN ILE SER VAL SER GLY GLY ASN VAL GGGAACATTTCAGTTTCAGGGGGGAATGT GGGAACATTTCAGTTTCAGGAGGGGAATGT 930 940	THR PHE ARG LEU ASN ALA SER SER  CACCTTCAGGCTTAACGCTTCATCCTCT  980  ASN GIN GIN THR PRO GLY VAL ILE ILE ASN SER  ASN GLA AACCCCTGGCGTAATTATAAATTC  AACCAGCAAACCCCTGGCGTAATTATAAATTC  AACCAGCAAACCCCTGGCGTAATTATAAATTC
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ER LYS GLY SER CAAAAGGGTCG 1040 CRE LHI ARC PHE CIII THR THR GLY SER THR LYS	AGCTTAAGATTTGAAACTACAGGTTCAACAAAA1050		THR LEU ASN ALA THR GLY GLY ASN ILE SER LEU A C T T T A A A C G C C A C T G G A G G C A A T A T A T C G C T			VAL VAL
1115	G A A		THR ACT			VAL
	T T T 1060	: : :	ALA G C C	1120	: : : :	1160 ILE GLY GLU GLY
SER T C G	A G A	LEU TTA	ASN A A C		MET A T G	CLU
SER LYS GLY SER T C A A A A G G G T C G 1040	TTA	ASN ASN ASP LEU A A T A A T G A T T T A 1100	LEU TTA		ILE ASP GLY MET A T T G A C G G G A T G	CLY
ER LYS CAAAA 1040	A G C1050	SN ASN ATAAT 1100	THR ACT	1110	ASP G A C	1160 ILE
SER T C A 10		ASN A A T	: :	•	ILE A T T	11(
ALA G C T		ILE A T A			G G C	
LYS HIS LEU ASN ALA AACACCTTAATGC' 1030		LEU TTA			GLU (GAAG	
LEU C T T 1030		PHE T T T 1090			LEU GIN VAL TGCAGGTTG	1150
HIS C A C		VAL GLY TCGGT			GLN C A G	
LYS HIS LEU ASN ALA TAAACACCTTAATGCT 1030		VAL GLY PHE LEU ILE AGTCGGTTTTTAATA			LEU GIN VAL GLU GLY CTTGCAGGTTGAAGGC	
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TTT...

GLY SER LYS LYS ALA ILE THR GLU ILE LYS GLY GGCTCCAAGAAAGCCATAACAGAAATCAAAGG1230 1240 1250	ASN VAL THR ILE ASN GLU ASN THR ASN  CATGTTACTATCAATGAAACACCAAC  1270  ALA THR LEU ILE GLY SER ASP PHE ASN ASP HIS COCACTCTTATCGGATTTAACGATCA COCACTCTTAACGGATTCA COCACTCTTAACGGATCA COCACTCTTAACGATCA COCACTCTTAACGATCA COCACTCTTAACGATCA COCACTCTTAACGATCA COCACTCTTAACGATCA COCACTCTTAACGATCA COCACTCTTAACGATCA COCACTCTTAACGATCA COCACTCTTAACGATCA COCACTCTTAACACA COCACTCTTAACACACACA COCACTCTTAACACACACACACACA COCACTCTAACACACACACACACACACACACACACACACA	LYS LYS PRO LEU ASN ILE LYS GLY ASP  FAAAAACCTTTAAATATAAAGGAGAT  1330  VAL VAL ASN ARG GLY ASN LEU THR ALA GLY GLY  GTCGTCAATAGAGCAACCTTACCGCTGGCG  GTCGTCAATAGAGCCAACCTTACCGCTGGCG  1350	ASN VAL ILE ASN ILE GLY GLY ASN LEU  A A T G T T A T C G C G C C C C C C C C C C C C C C C
	THR A C T 7 1270	PRO C C T 1 1330	ILE A T C <i>1</i> 1390
	ASN VAL	LYS LYS A A A A A C	ASN VAL
	ASI A A A	LY.	ASI A A S

THR ASN PHE THR PHE ASN VAL GLY GLY  CACAAATTTCACTTTTAATGTAGGCGGC  1450  LEU PHE ASN ASN LYS GLY ASN SER ASN ILE SER  TTGTTTAACAACAAGGCAATTCAAATATCTC  1470  1480  1500	ILE ALA ARG GLY GLY ALA LYS PHE LYS  C A T T G C T A G G G G C T A A T T T A A A  1510  ASP ILE ASN ASN THR SER SER LEU ASN ILE THR  G A T A T C A A T A C A C C G T A G C T T A A A T A T T A C A C A C A G T A G C T T A A A T A T T A C A T A C A C A G T A G C T T A A A T A T T A C A T A C A C A G T A G C T T A A A T A T T A C A T A T C A T A T	THR ASN SER ASP THR TYR ARG THR CACCAACTCCGACTTACCGTACC 1570 ILE ILE GLU GLY ASN ILE THR ASN LYS ALA GLY A T T A T A G A A G G T A A T A T A A C C A A C A A G C A G 1620 1620	ASP LEU ASN ILE ILE ASP ASN LYS GLY TGATTTGAATATCATTGATAAAGGT 1630 1640
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SUBSTITUTE SHEET (RULE 26)

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ILE SER ATCTC 1680	ILE THR TAAC 1740	ASN LEU A T C T 1800
ASN ALA GLU ILE GIN ILE GLY GLY ASN ILE SER A A C G C T G A A T C C A A T T G G C G G C A A C T C T C 1670 1680	GCAAAAGAAGTAACCTCACGATTTCC  GCAAAAAAAGGTAACCTCACGATTTCC  1690  SER ASP LYS ILE ASN ILE THR LYS GIN ILE THR  TCCGATAAAATCAATACCAAACAGATAAA  1740	ILE LYS LYS GLY VAL ASN GLY GLU ASN  A A T C A A G A A C G G A G A G A A C  1750  SER ASP SER THR LYS SER GLN ALA ASN LEU  T C T G A T T C A A G T A C G A A A A G T C A A G C C A A T C T  T C T G A T T C A A G T A C G A A A A G T C A A G C C A A T C T  1770  1780

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AAGATAGTAGT 1880 ASN LEU THR ILE GLY ASN SER ASP SER AATTTAACTATTGGTAATAGTGATGC	1890 1920 1920 1920 1920 1920 1920 1920 19	ASN ASN VAL LYS ASP SER LYS 1115 SEK ALA ASP A A C A A T G T T A A G A T T C A A A A T C T G C T G A 19801950	GLY HIS LYS VAL THR LEU ASN SER LYS CGGTCACAAGGTGACACTAAATAGCAAA 1990 VAL LYS THR LEU SER ASP ASN ASN THR GTGAAAACACTTAGTGATAATGATAACACAC	TACCGGT
AGCAAAGATTGTAGCTAAA(1880)	SER ALA LYS THR AGCGCTAAAACA 1930 194	<u>P</u>	HIS LYS VAL THR LEU CACACTA? 1990 2000 G	GLY SER ASP ASN GGCAGTGACAACA 2050
AGCAAAG	ASN THR CAATACT?		GGTCAC	GLU GLY GLY TGAAGGTGGCA

	233		
ASIN A A A 2100	THR C A C 2160	. GLY A G G 2220	ASP C G A 2280
VAL 3 T A 1 2.	THR ACCA 21	THR GLY ACAGG 2220	GLY 3 G C (
GLU 3 A A (	ILE A T T A	HIS CATA	ALA GLY
ASP VAL GLU BATGTAGAAC 2090	GLY GLY 5 G A G G G A 2150	THR ALA CCGCTC 2210	ALA 3 C A (
ASP V 3 A T G 2090	GLY G 3 G A G 2150	THR A ACCG ( 2210	VAL 7 3 T G G 2270
LYS A A A C	ASN A A T (	ILE A T A A	ILE ATTG
LEU THR ILE THR ALA LYS ASP VAL GLU VAL AST TTAACTACTGCAAAGATGTAGAAGTAAA 2070 2080 2100	ACAAAACAGTG 2120 ASN VAL SER ALA ALA ASN GLY GLY ILE THR THE AACGTCTCTGCGCAAATGGAGGATTACCAC 2150 2150 2140 2150	TE ASN ALA THR  TTAATGCAACC 2180 ALA GLY ASN VAL GLU ILE THR ALA HIS THR GLY GCCGGTAACGTGAAAACAGG 3200 2210	TEGUSER LYS  TTGAGTCCAAG  2240  PRO GLY SER VAL THR ILE VAL ALA GLY GLY ASI  CCTGGCTCTGTGACAATTGTGCCAGGCGA  2250
THR ILE THR CTATTACT G 2080	  ALA G C G ( 2140	  VAL 3 T G (	  VAL G T G A
ILE A T T .	HIS LYS THR VAL C A C A A A A C A G T G 2120 ASN VAL SER A A A C G T C T C T G G 2130	ILE ASN ALA THR A T T A A T G C A A C C 2180 ALA GLY ASN V G C C G G T A A C G' 2190	ILE GLU SER LYS A T T G A G T C C A A G 2240 PRO GLY SER VI C C T G G C T C T G 7
THRACT	THR ACA VAL GTC	ALA G C A GLY	GLU SER LYS AGTCCAAG PRO GLY SER CTGGCTCT 50
LEU T T A A	ES LYS A C A A A 2120 A A B A A 2120 A A B A C A A A C A A A C A A A C A A C A A A C A A C A A A C A A A C A A A C A A A C A A A C A A A C A	LE ASN T T A A T 2180 ALA G C C (	GLU G A G 0 PRO C C T (
LEU	HIS LYS C A C A A 2120 ASN A A (	ILE ASN A T T A A 2180 ALA G C (	ILE GLA A T T G A 2240 PRC C C
		THR A C C	
	THR ACTI	THR ACAA	G G C
	ILE A T T A 2110	GLY G G T A 2170	ILE GIN GLY TCCAAGGCO
	ASN ASN ILE THR SER CAACAATATTACTTCT 2110	LYS THR GLY THR THR TAAAACAGGTACAACC 2170	SER ILE GIN GLY GLY CAGTATCCAAGGCGGA 2230
	ASN A A C	LYS AAAA	SER AGTA
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### FIG.27L

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ALA . G C 2340	GLN ' C A 2400	SER ' A G 2460	
ALY GT (	SER GIN GTCA 2400	ASN . A T A 24	
FF C G	R A A	R ZTA	
SE IAG	THR SER	A A C	
ASIN A A 7	THR AC'	ALA G C 7	
ALA A. G C A A 7 2330	ILE THR T TAACCA 2390	LYS P AAAG 2450	
2300 ASN ALA VAL THR VAL THR ALA ASN SER GLY ALA A A C G C C G T T A C T G C A A T A G C G G T G C 2310 2320 2340	LY SER THR ILE GCTCTACAATT 2360 LYS GLY THR GLU SER ILE THR THR SER GLA AAAGGAACCGAGAGTATAACCACTTCAAGTCA 2300 2400	TAAAATTTCC 1AAAATTTCC 2420 GLY LYS THR VAL ASN VAL LYS ALA THR ASN SET GLY LYS THR VAL ASN VAL LYS ALA THR ASN SET GGCAAGTAAACGTTAAAGCAACTAATAG	
VAL G T T	SER :	ASN A A C	
THR A C T 2320	  GLU 3 A G 2380	  VAL G T A 2440	
ASN ALA VAL THR A A C G C C G T T A C T C 2310 2320	LEU THR LEU ALA GLY SER THR ILE ATTAACCACTTTGGCAGGCTCTACAATT 2350 2360 LYS GLY THR GLU AAAGGAACCGAGA	T A A A A T T T C C 2420 GLY LYS THR V GGCAAGACAG' 2430	LEU THR GIN ALA ASP SER LYS ILE TTTAACCACCCAAGCAGACTCAAAATT 2470 2480
ALA G C C	THR ACAA GLY 'G GAA	ILE ATTT LYS AAGA	LYS A A A A
. ASN . A A C . 2310	JY SER  3 C T C T A 2360 LYS A A A G 2370	.Y LYS T A A A A 2420 GLY  G G C A G G C A 2430	SER TCAA
2300 A A 23	ALA GLY 5 C A G G C 236	ASN ILE GLY GLY A A T A T C G G C G G T P 2420 2420 G	THR THR GLN ALA ASP ACCACCAAGCAGACT 2470
	ALA G C A	G G C	ALA G C A
	LEU TTG	ILE A T C	GLN C A A
2290	THR THR LEU CCACTTTG( 2350	ASN A A T 2410	THR A C C 2470
	THR ACC	SER GLY	THR ACC
	LEU TTAA	SER GLY ASN ILE GLY GLY A TOTOGGCGG 2410	LEU
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VAL

ACCAA

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SER A A G 2520	GLU G A 2580	SER CG 140
~	GCGGTACAATT  GCGGTACAATT  2540  SER GLY GLY THR VAL GLU VAL THR ALA THR GLU TCTGGTGGCACAGAAGTTACCGCGACCGA TCTGGTGGCACAGAAGTTACCGCGACCGA 2550	LA GLY SER THR CAGGCTCTACG 2600 ILE THR GLY THR GLU SER VAL THR THR SER SER ATTACTGGAACCGAGGCGTGACCACTTCAAG ATTACTGGAACCGAGAGAGCGTGACCACTTCAAG
VAL THR GTAAC	ALA 3 C G 7	THR ACT 1
ASN A A T (	THR ACC(	THR ACCI
ALA AS G C T A A 2510	VAL TH GTTAC 2570	VAL TH GTGAC 2630
GLU GAG	GLU GAA	SER A G C
CEN GGC	VAL G T A	GLU GAG
GLU G A A 2500	 THR A C A 2560	 THR A C C 2620
THRACT	GLY GLY THR ILE  G G C G G T A C A A T T  2540  SER GLY GLY TE T C T G G T G G C A (2)	ALA GLY SER THR C A G G C T C T A C G 2600 ILE THR GLY TI A T T A C T G G A A (
ALA G C G	THR ACA GLY GGT	SER TCT THR ACT
GAA2490	JIY GLY G C G G T 2540 SER T C T 2550	LA GLY C A G G C 2600 ILE A T T
	<sup>ტ</sup> ტ	ALA GI G C A G C 2600 II A T
	ILE A T T	GLN C A A
	ILE A T A	THR ACC
	SER A G C 2530	THR A C C 2590
	LYS THR SER ILE ILE A A A C A A G C A T A A T C 2530	GLY LEU THR THR GLN GTTTAACCACCCA 2590
	LYS THR SER ILE ILE CAAACAAGCATAATT 2530	GLY LEU THR THR GLN ALA GLY SER THR AGGTTTAACCACCCAAGCAGGCTCTACG 2590 ILE THR GLY T ATTACTGGAA

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; A C 2880 G

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GAGGA

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... G C A *1* ...2850

GLY

GLY

ASP LEU ILE THR LYS SER GLY SER GLU	CTAAAT	2710 2720	ILE LYS ALA THR ALA GLY GLU VAL ASN VAL THR	A T T A A G C A A C G G C G G C G A G G T G A A T G T A A C	2730 2740 2750		SER ALA THR GLY THR ILE ASP GLY THR	AAGTGCAACAGGTACAATTGACGGTACG	2770 2780	ILE SER GLY ASN THR VAL ASN VAL THR ALA ASN	ATTTCCGGTAATACGGTAATGTTACAGCAAA	282 2810 2810 2820	THR GLY ASP LEU THR VAL GLU ASP ALA	TACTGGCGATTTAACTGTTGAAGATGCC	2830 2840	
				AAC	2760					A ASIN	AAA	2820				
			W	l G T						AL	A G C					
			ASIN	AAJ						强	ACA					
			VAL	GT G	0					VAL	GTT	0.				
			CITO	GAG	275					ASIN	AAT	281				
			GLY	J 5 5						VAL	GTA					
			ALA	G C G						当	ACG					
•	•	•	当	ACG	2740		:	:	:	ASIN	AAT	2800	:	:	:	
CIN.	GAG.	•	ALA	GCA			当 到	ACG.	•	GLY	GGT		ALA.	GCC.	•	
SER	TCA		LYS	AAA		;	GLY	G G T		SE	J L L		ASP	GA T		
GLY	GGT	50	II.E	ATT	:730	,	ASP	G A C	200	IIE	ATT	1790	GLU	GAA	. 01	
SER	TCC	272	:	:		1	IIE	A T T	278	:	:	2	VAL	GTT	284	
LYS	AAA						置	ACA					国	ACT		
開	ACT						GLY	GGT					LEU	TTA		
H	ATT	2710					開	ACA	2770					GAT	2830	
E	ΤΤΑ							GCA					GLY	G G C		
ASP	AGAT						ğ	AAGT					開	TACT		
					0		~ T I	~~ 1	TE	eur	-67	· /DI	 26	`		

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TTAACC... G G C A A A 7 2900 TCG 段 ACA 盟 ACT( CTA LEU  $\mathcal{O}$ 

THR LYS ALA SER SER SER ILE THR SER ALA ASN A C T A A G C T A G T T C A A C C A T T A C T T C A A C T A A A C T L C A G C T A A A 2920 2930 2940	ASN LEU SER ALA LYS ASP  A A C C T T C A G C T A A G G A T  2960  GLY SER ILE GLY GLY ASN ILE ASN ALA ALA ASN 8500 650	ASN THR GLY ALA LEU  A A T A C T A C A G G C G C T C T A  3020  THR VAL LYS GLY SER SER ILE ASN ALA ASN  A C T A C C G T G A A G G G T T C A A G C A T T A A C G C A A A  3050  3050	LEU VAL·II.E ASN ALA LYS  TGGTTATTAACGCAAAA 3080 ASP ALA GLU LEU ASN GLY GLU ALA SER GLY ASN GACGCTGAGCTAAATGGTGAGGCATCAGGTAA 3120
	ASN GIN VAL ASN LEU SER TAACCAGGTAAACCTTTCA 2950 2950	THR 1	□ <b>4</b> :

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C T C 3180	LYS A A A 3240	PRO A C C 3300	
THR 1 C C 1 31	SER FCAA 32	ASP VAL LYS TYR ILE GIN 3 A T G T G A A A T A C A T T C A A C 3290	
THR '	ILE ATTT	T T C	
ALA 1	E ]	R J	
ILE AI ATCGO 3170	IN II 1 T A T 3230	YS TY A A T <i>P</i> 3290	
ILE A A T	ASN 3	LYS RAA 3	
SER VAL	LEU TTP	VAL G T G	
ALA THR ASN ALA  CAACCAACGCA 3140 ASN GLY SER GLY SER VAL ILE ALA THR THR SET ASN GLY SER GLY SER VAL ILE ALA THR THR SET ASN GLY SER GLY SER 3160 3150 3150	THR GLY ASP LEU CTGGGGATTTA 3200 ILE THR ILE ASN GLY LEU ASN ILE ILE SER LY ATCACAATAAATGGATTAAATATCATTTCAAA 3240 3220	AL LEU LEU LYS  TACTGTTAAAA 3260 GLY VAL LYS ILE ASP VAL LYS TYR ILE GIN PRC GGCGTTAAAATTGATGTGAAATACATTCAACC3270	
ALA THR ASN ALA  C A A C C A A C G C A  3140  ASN GLY SER GLY  A A T G G C T C C G G C A  A A T G G C T C C G G C A  3150	  ASN A A T C	AL LEU LEU LYS TACTGTTAAAA 3260 CLY VAL LYS ILEGGCGTTAAAATTG	
ALA THR ASN ALA  C A A C C A A C G C A  3140  ASN GLY SER G A A T G G C T C C G 3 3150	THR GLY ASP LEU  C T G G G G A T T T A  3200 ILE THR ILE A A T C A C A A T A A 3210	VAL LEU LEU LYS 3 T A C T G T T A A A A 3260 GLY VAL LYS II G G C G T T A A A A S 33770	SP GLU VAL ILE A T G A A G T A A T T 3320
N A CG CTC	P LL TT TT S II	U L AA. TAI	
AS CAA GL GL	AS G G A THI	LEG TAN	VAJ A G T
LA THR C A A C 3140 A A SI A A SI A A SI A A SI 50	THR GLY ASP LEU CTGGGGATTT 3200 ILE THR ILE ATCACAATA3210	AL LEU TACT ( 3260 GG ( GG (	ASP GLU VAL 3ATGAAGTAA 3320
ALA G C A 31		VAL LJ 3 T A C ' 3260 GI G C	
HIS THR VAL VAL ASN ACCATACAGTAGTGAATG	SER ARG VAL ASN ILE 7 A A G C A G A G T G A A C A T C A 3190	ASN GLY ILE ASN THR VAAACGGTATAAACCGG	GLY ILE ALA SER VAL A GGGTATAGCAAGCGTAG 3310
VAL ASN STGAAT	ASN A A C A	ASN THR	SER AGCG
VAL G T A G 3130	VAL 23 T G A 3190	ILE 7 A T A A 3250	ALA S S C A A 3310
THR VACAGO	ARG VAL 1 G A G T G A 3190	7 II 7 32 32 32	ILE AI TAGO
TH LAC	ARC	GLY	ILE
HIS CATA	SER AGCA	ASN AACG	GLY G G T
S	A	A	Ŋ

# FIG.27Q

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ASP A G A 3360	-4	SER A A G 3480	CYS A T G 3540
LYS A A A (	PHE I T T G	SER I C A A 34	ILE (
VAL 3 T A A	ARG	PRO	THR 1 C A A
LYS A A G G	VAL	ARG A G A C	ALA C A A
GLU I A G A 3350	ALA VAL CTGTA(	THR 7 CCA 3470	3530 3530
LEU GLU 7 T G A G A 3350	SER SER	THR THR 1 CAACCA 3470	GLY ASN GLY ALA GCAATGGTGCAA
TCC	VAL 3 T A A	PHE '	ILY A
ARG ILE CGCATCC 3340	  GLY 3 G C G	  GLU 1 3 A G T 3460	  ILE ( A T C G 3520
GLU ALA LYS ARG ILE LEU GLU LYS VAL LYS ASI GAAGCGAAACGCATCCTTGAGAAGGTAAAGA 3330		LE THR ILE ASN  T A C G A T T A A T  3440  THR GIN ASN GLU PHE THR THR ARG PRO SER SE  A C A C A A A T G A G T T T A C A A C C A G A C C A T C A A G  3480	LU GLY LYS VAL A A G G T A A G G T A 3500 CYS PHE LEU ILE GLY ASN GLY ALA THR ILE CY: T G T T T C T T A A T C G C C A T G G T G C A A C A A T A T G 3510
ALA ]	ALA LEUGCTTA	ILE ALT TA ALT ALT ALT ALT ALT ALT ALT ALT	LYS A A G G A A G G G PHE I
GLU 7 S A A G 330	GLU SAAG	THR CA A C G A D D D D D D D D D D D D D D D D D D	GLY IGTAO
G A	GLU ARG GLU SAAAGAGAAC 3380 ALA GCTA	ILE THE A T T A C 3440 THR A C	310 GL) A A G G 3500 CYS T G3510
	A A A A	ALA CCA	THR ILE SER GLU CAATTTCTGAA 3490 350
	GLU A A G	ATG	T T T T T T T T T T T T T T T T T T T
	ASP GLU SATGAA( 3370	ASN , 3430	THR A C A A 3490
	SER CTO	GLU PRO ASN ALA ILE THR ILE ASN  TGAGCCAAATACCATTACGATTAAT 3430 3440 THR GIN ASN GI ACACAAATG3.	GIN VAL THR ILE SER GLU GLY LYS VAL  TCAAGTGACAATTTCTGAAGGTAAGGTA 3490 3500 CYS PHE LEU II TGTTTCTTAAG
	LEU TAT	GLU A G C	GIN (
	<b>:</b> <b>:</b> -	- B	J C

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FIG.27R

CACCAATATTGCTGATATTGAGCGG 3550

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09	120	180	240	300	356	404	452
ACAGOGITICT CITAATACTA GIACAAACCC ACAATAAAAT ATGACAAACA ACAATTACAA	CACCITITIT GCAGICIAIA IGCAAAIAIT IIAAAAAAIA GIAIAAAICC GCCAIAIAAA	ATGGTATAAT CTITICAICTT TCATCTTTCA TCTTTCATCT TTCATCTTTC ATCTTTCATC	TITICATETIT CATETITICAT CITICATETIT TCATETITICA TETITICATET TICATETITIC	ACATICOCOTIC ATGAACOCGAG GGAAGGGAGG GAGGGGCAAG AATGAAGAGG GAGCTGAACG	AACGCAAATG ATAAATAAT TTAATTGTTC AACTAACCTT AGGAGAAAT ATG AAC Met Asn	AAG CTA TAT CGT CTC AAA TTC AGC AAA CGC CTG AAT GCT TTG GTT GCT Lys Leu Tyr Arg Leu Lys Phe Ser Lys Arg Leu Asn Ala Leu Val Ala 5	GTG TCT GAA TTG GCA CGG GGT TGT GAC CAT TCC ACA GAA AAA GGC AGC Val Ser Glu Leu Ala Arg Gly Cys Asp His Ser Thr Glu Lys Gly Ser 20

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200	548	596	644	692	740
GAA AAA CCT GCT CGC ATG AAA GTG CGT CAC TTA GCG TTA AAG CCA CTT Glu Lys Pro Ala Arg Met Lys Val Arg His Leu Ala Leu Lys Pro Leu 35 40 45	TCC GCT ATG TTA CTA TCT TTA GGT GTA ACA TCT ATT CCA CAA TCT GTT Ser Ala Met Leu Leu Ser Leu Gly Val Thr Ser Ile Pro Gln Ser Val 55 60	TTA GCA AGC GGC TTA CAA GGA ATG GAT GTA GTA CAC GGC ACA GCC ACT Leu Ala Ser Gly Leu Gln Gly Met Asp Val Val His Gly Thr Ala Thr 70 75 80	ATG CAA GTA GAT GGT AAT AAA ACC ATT ATC CGC AAC AGT GTT GAC GAT Met Gln Val Asp Gly Asn Lys Thr Ile Ile Arg Asn Ser Val Asp Asp 85	ATC ATT AAT TGG AAA CAA TTT AAC ATC GAC CAA AAT GAA ATG GTG CAG Ile Ile Asn Trp Lys Gln Phe Asn Ile Asp Gln Asn Glu Met Val Gln 100	TITY TITA CAA GAA AAC AAC TCC GCC GTA TTC AAC CGT GTT ACA TCT Phe Leu Gln Glu Asn Asn Asn Ser Ala Val Phe Asn Arg Val Thr Ser 115
			T (DIU E 06)		

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788	836	884	932	086	1028			
AAC CAA ATC TCC CAA TTA AAA GGG ATT TTA GAT TCT AAC GGA CAA GTC Asn Gln Ile Ser Gln Leu Lys Gly Ile Leu Asp Ser Asn Gly Gln Val 135	TIT TITA ATC AAC CCA AAT GGT ATC ACA ATA GGT AAA GAC GCA ATT ATT Phe Leu Ile Asn Pro Asn Gly Ile Thr Ile Gly Lys Asp Ala Ile Ile 150	AAC ACT AAT GGC TIT ACG GCT TCT ACG CITA GAC AITT TCT AAC GAA AAC Asn Thr Asn Gly Phe Thr Ala Ser Thr Leu Asp Ile Ser Asn Glu Asn 175	ATC AAG Ile Lys 180	GCT GAA ATT GTG AAT CAC GGT TTA ATT ACT GTC GGT AAA GAC GGC AGT Ala Glu Ile Val Ash His Gly Leu Ile Thr Val Gly Lys Asp Gly Ser 200 210	GTA AAT CTT ATT GGT GGC AAA GTG AAA AAC GAG GGT GTG ATT AGC GTA Val Asn Leu Ile Gly Gly Lys Val Lys Asn Glu Gly Val Ile Ser Val 225			
	SUBSTITUTE SHEET (RULE 26)							

# FIG.28D

1220 1076 1172 1124 ATC AGC Ile Ser Ser 290 GAA AAT Asn Pro Glu Asn Asp GAT GGT AAC A GCT Ala ACC Thr 240 AIC 11e GCG Ala 255 ICI Leu Ser CII AAA Lys Ala 8 Gly 270 8 GGT AAA Gly Lys Lys 285 AIT Ile Lys Gln CAA GCC AAA AGC Ala 99 Ser G1yCAA Gln Phe GCA Ala 235 TAC TYYCGA AAC ( Arg Asn ( Ile Fer ACT Thr 250 AIT CIC Asp 265 Ile ATT GAI TTA E AIT 11e 280 GLYACC Ser Thr 8 ACT 7 E S CIG Pro AIT Asn 9 Ala AAC AAT Ser 230 Asn AGC occ orc Ala Val 260 EJ EJ GlyATA Ala Ile 245 8 CGT GG ATA Ile Arg Gly AAT GAI Val 275

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PCT/CA99/00938

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GGT GLY

Glu 305

Lys

Ala

Ser

Fen

GIT Val 300

AIT 11e

GLY

Ser AGC

Lys 295

Asp

Lys

Ser

AAT. Asn

9

AAA

GAI

GTA

GAG

AAA

CIT TOC GCC

Lys

Gln , 320

CAPA

GCT CAA AAT CAG Ala Gln Asn Gln

TCC Ser 315

GTA ATT '

GGT GLY

GGC Gly

AIT

GAA Glu

999

GAA

Ala

#### 189/235

1364		1412	1460	1508	1556	1604
<del>`</del> i		Ä	↔	$\leftarrow$	<b></b>	$\leftarrow$
TIG ATG ATT ACA GGC GAT AAA GTC ACA	Lys Leu Met 11e 'inr Gly Asp Lys val 11m Leu Lys 11m 325	GIT ATC GAC CIT TCA GGT AAA GAA GGG GGA GAA ACT TAC CIT GGC Val Ile Asp Leu Ser Gly Lys Glu Gly Gly Glu Thr Tyr Leu Gly 340	GAC GAG CGC GAA GGT AAA AAG GGC ATT CAA TTA GCA AAG AAA Asp Glu Arg Gly Glu Gly Lys Lys Gly Ile Gln Leu Ala Lys Lys 360	TCT TTA GAA AAA GGC TCA ACC ATC AAT GTA TCA GGC AAA GAA AAA Ser Leu Glu Lys Gly Ser Thr Ile Asn Val Ser Gly Lys Glu Lys 375	GGA CGC GCT ATT GTG TGG GGC GAT ATT GCG TTA ATT GAC GGC AAT Gly Arg Ala Ile Val Trp Gly Asp Ile Ala Leu Ile Asp Gly Asn 390	AAC GCT CAA GGT AGT GGT GAT ATC GCT AAA ACC GGT GGT TTT GTG Asn Ala Gln Gly Ser Gly Asp Ile Ala Lys Thr Gly Gly Phe Val 405
98	Gly	GCA Ala	GGT G1y 355	ACC Thr	99C Gly	AIT Ile

### FIG.281

GAG ACG 1 Glu Thr 9 420	OCC AAA ( Ala Lys ( 435	ACA GCA ( Thr Ala (	GGG AAT ? Gly Asn S	ACA AAC A Thr Asn 1	ATC ACT C Ile Thr A
TCC GGG Ser Gly	GAG TGG Glu Trp	GGA CGC Gly Arg	AGT GCC Ser Ala 470	ACA ACT Thr Thr 485	GCT AAT Ala Asn
CAT His	TTG	AGC Ser 455	AGC	CTT	caa coc Gln Arg
GAT TTA Asp Leu 425	TTA GAC CCG Leu Asp Pro	AAT ACT 7 Asn Thr 9	ACC CCA Thr Pro	GAG AGT Glu Ser	OC ATC Arg 11e 505
TIC	GAC CCG	ica Ser	A AAA o Liys	r ATA r 11e 490	TAT Tyr
AIC Ile	GAT Asp	GAA	CGA A Arg A 475	CTA A Leu L	GIC Val
AA GA ys As	AAT GTA Asn Val 445	GAC GAT ASP ASP 460	AC AA SIN Liy	AA AA ys Ly	AAT AGC Asn Ser
C AAT p Asn 430		T GAA p Glu	AAA CGA AAC AAA GAA AAG Lys Arg Asn Lys Glu Lys 475	ATA CTA AAA AAA GGT ACC Ile Leu Lys Lys Gly Thr 490	c 100 r Ser 510
AAA GAC AAT GCA ATT GTT Lys Asp Asn Ala Ile Val 430	TCT ATT AAT GCA Ser Ile Asn Ala	GAA TAC ACG Glu Tyr Thr	AAG ACA Lys Thr 480	ACC TITT Thr Phe 495	ATT AAT Ile Asn
r GIT	: GCA 1 Ala	3 GGA : Gly 465	A ACA Thr	GIT Val	TTA Leu
GAC Asp	GAA Glu 450	TCC	TTA Leu	AAC Asm	TCC Ser
1652	1700	1748	1796	1844	1892

### FIG.28(

1940	1988	2036	2084	2132	2180
AAT GGC AGC TTA ACT CTT TGG AGT GAG GGT CGG AGC GGT GGC GGT GTA ASN Gly Ser Leu Thr Leu Trp Ser Glu Gly Arg Ser Gly Gly Gly Val 515 520	GAG ATT AAC AAC GAT ATT ACC ACC GGT GAT GAT ACC AGA GGT GCA AAC	TTA ACA ATT TAC TCA GGC GGC TGG GTT GAT GTT CAT AAA AAT ATC TCA	CTC GGG GCG CAA GGT AAC ATA AAC ATT ACA GCT AAA CAA GAT ATC GCC	TITY GAG AAA GGA AGC AAC CAA GIC ATTY ACA GGT CAA GGG ACTY ATTY ACC	TCA GGC AAT CAA AAA GGT TTT AGA TTT AAT AAT GTC TCT CTA AAC GGC
	Glu Ile Asn Asp Ile Thr Thr Gly Asp Asp Thr Arg Gly Ala Asn	Leu Thr Ile Tyr Ser Gly Gly Trp Val Asp Val His Lys Asn Ile Ser	Leu Gly Ala Gln Gly Asn Ile Asn Ile Thr Ala Lys Gln Asp Ile Ala	Phe Glu Lys Gly Ser Asn Gln Val Ile Thr Gly Gln Gly Thr Ile Thr	Ser Gly Asn Gln Lys Gly Phe Arg Phe Asn Asn Val Ser Leu Asn Gly
	545	550 555	565 575	580 585	595 610

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GCC AGC GGA CTG CAA TTC ACC ACT AAA AGA ACC AAT AAA GLY Ser Gly Leu Gln Phe Thr Thr Lys Arg Thr Asn Lys ACA AAT AAA TTT GAA GGG ACT TTA AAT ATT TCA GGG AAA Thr Asn Lys Phe Glu Gly Thr Leu Asn Ile Ser Gly Lys G30  TCA ATG GTT TTA CCT AAA AAT GAA AGT GCA TAT GAT AAA Ser Met Val Leu Pro Lys Asn Glu Ser Gly Tyr Asp Lys 645  CCC ACT TAC TGG AAT TTA ACC TCC TTA AAT GTT TCC GAG ARG Thr Tyr Trp Asn Leu Thr Ser Leu Asn Val Ser Glu 660  TTT AAC CTC ACT ATT GAC TCC AGA GGA ACC GAT AGT CCA ACC CAG CAG ACC CAT AGT CACA ACC CAG CAT AGT CACA ACC CAG CAT AGT CACA ACC CAG CAT ACT TAC ACA ACC CAG CAT ACT CACA ACC  AC	2228	2276	2324	2372	2420	2468
ACT Thr Thr AIC IIle AIC CLA GGA GGA GGA GGA GGA GGA GGA GGA GGA G	AGC GGA CTG CAA TTC ACC ACT AAA AGA ACC AAT AAA TAC Ser Gly Leu Gln Phe Thr Thr Lys Arg Thr Asn Lys Tyr 625	TIT GAA GGG ACT TTA AAT ATT TCA GGG AAA GTG Phe Glu Gly Thr Leu Asn Ile Ser Gly Lys Val 635	TTA CCT AAA AAT GAA AGT GGA TAT GAT AAA TTC Leu Pro Lys Asn Glu Ser Gly Tyr Asp Lys Phe 650	TAC TOG AAT TTA ACC TCC TTA AAT GTT TCC GAG AGT Tyr Trp Asn Leu Thr Ser Leu Asn Val Ser Glu Ser 665	TTT AAC CTC ACT ATT GAC TCC AGA GGA AGC GAT AGT GCA GGC Phe Asn Leu Thr Ile Asp Ser Arg Gly Ser Asp Ser Ala Gly 685	ACC CAG CCT TAT AAT TTA AAC GGT ATA TCA TTC AAC AAA GAC Thr Gln Pro Tyr Asn Leu Asn Gly Ile Ser Phe Asn Lys Asp 705

### FIG.28I

2516 2564 2612 2660 2708 2756 CTT CTC Leu Leu Asn AAA Lys 770 8 G1yAAT GCC AAG Lys Phe Ser TCA Ser 785 Asn GIT ATA AAT VAl Ile Asn 3 TITT AAA ACT The Phe Lys Thr Ile 720 ACA Thr Ser TIA Leu 800 JE L GAC Asp Phe Ala 735 TTPA ACT Thr Asp 750 TIT Phe TYTGAT TAC Fen AGA Arg Asn AAC AAT Asn GGG GGG AGT GTT Gly Gly Ser Val GIYA Val 765 GAG AAA GAT Lys Asp Val TTA I Leu 7 TIG GGT Gly CIC Leu GGG TCA AGT Caly Ser Ser I CAA ACC CCC (Glu Thr Pro ( AGA Arg 715 Ser AGT Glu 795 Ala G1yCGA AAT GCA Ser 730 ATA GGA G1y 745 TCA Ser Glu Arg Asn TAT Tyr 100 Ser ACA Thr ATA AAT AAG GIC Ile Asn Lys TIC Phe Val 760 Asn 1 Val GAA GIJ TCA Ser 775 AAC 9 Gly Ser TCA Ser Val GIJ Asn Val ACT Thr 790 710 Asn AAT 999 Ile TIT AAT Gly 725 JGC AAA Lys Ser TIT. AAC Asn Phe Ile ATA TCA Ser Phe 740 Pro SEA PER 3cc Ala 755

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### FIG.28,

2804	2852	2900	2948	2996	3044
ACC GGA GGC AAC ATA ACA CTT TTG CAA GTT GAA GGC ACC GAT GGA ATG	AIT GGT AAA GGC ATT GTA GCC AAA AAA AAC ATA ACC TTT GAA GGA GGT	AAC ATC ACC TITT GGC TCC AGG AAA GCC GTA ACA GAA ATC GAA GGC AAT	GIT ACT AIC AAT AAC AAC GCT AAC GIC ACT CIT AIC GGT TCG GAT TITT	GAC AAC CAT CAA AAA CCT TTA ACT ATT AAA AAA	AGC GGC AAC CTT ACC GCT GGA GGC AAT ATT GTC AAT ATA GCC GGA AAT
Thr Gly Gly Asn Ile Thr Leu Leu Gln Val Glu Gly Thr Asp Gly Met	Ile Gly Lys Gly Ile Val Ala Lys Lys Asn Ile Thr Phe Glu Gly Gly	Asn Ile Thr Phe Gly Ser Arg Lys Ala Val Thr Glu Ile Glu Gly Asn	Val Thr Ile Asn Asn Asn Ala Asn Val Thr Leu Ile Gly Ser Asp Phe		Ser Gly Asn Leu Thr Ala Gly Gly Asn Ile Val Asn Ile Ala Gly Asn
805	820	835	855		885

SUBSTITUTE SHEET (RULE 26)

### FIG.28k

3092	3140	3188	3236	3284	3332
CIT ACC GIT GAA AGT AAC GCT AAT TIC AAA GCT AIC ACA AAT TIC ACT Leu Thr Val Glu Ser Asn Ala Asn Phe Lys Ala Ile Thr Asn Phe Thr 900	TITY AAT GTA GGC TTG TTT GAC AAC AAA GGC AAT TCA AAT AITT TCC Phe Asn Val Gly Gly Leu Phe Asp Asn Lys Gly Asn Ser Asn Ile Ser 925	ATT GCC AAA GGA GGG GCT CGC TTT AAA GAC ATT GAT AAT TCC AAG AAT Ile Ala Lys Gly Gly Ala Arg Phe Lys Asp Ile Asp Asn Ser Lys Asn 945	TITA AGC ATC ACC ACC AAC TCC AGC TCC ACT TAC CGC ACT ATT ATA AGC  Leu Ser Ile Thr Thr Asn Ser Ser Ser Thr Tyr Arg Thr Ile Ile Ser  955 955	GGC AAT ATA ACC AAT AAA AAC GGT GAT TTA AAT AIT ACG AAC GAA GGT Gly Asn Ile Thr Asn Lys Asn Gly Asp Leu Asn Ile Thr Asn Glu Gly 970	AGT GAT ACT GAA ATG CAA ATT GGC GGC GAT GTC TCG CAA AAA GAA GGT Ser Asp Thr Glu Met Gln Ile Gly Gly Asp Val Ser Gln Lys Glu Gly 980
	20	חכ שוטוו כם	EET (NULE 20	,	

## FIG.28L

3380	3428	3476	3524	3572	3620
AAT CTC ACG ATT TCT TCT GAC AAA ATC AAT ATT ACC AAA CAG ATA ACA Asn Leu Thr Ile Ser Ser Asp Lys Ile Asn Ile Thr Lys Gln Ile Thr 995	ATC AAG GCA GGT GTT GAT GGG GAG AAT TCC GAT TCA GAC GCG ACA AAC Ile Lys Ala Gly Val Asp Gly Glu Asn Ser Asp Ser Asp Ala Thr Asn 1025	AAT GCC AAT CTA ACC ATT AAA ACC AAA GAA TTG AAA TTA ACG CAA GAC A ASn Ala Asn Leu Thr Ile Lys Thr Lys Glu Leu Lys Leu Thr Gln Asp 1030 1035	CTA AAT ATT TCA GGT TTC AAT AAA GCA GAG ATT ACA GCT AAA GAT GGT Leu Asn ile Ser Gly Phe Asn Lys Ala Glu ile Thr Ala Lys Asp Gly 1045	AGT GAT TTA ACT ATT GGT AAC ACC AAT AGT GCT GAT GGT ACT AAT GCC Ser Asp Leu Thr Ile Gly Asn Thr Asn Ser Ala Asp Gly Thr Asn Ala 1060	AAA AAA GTA ACC TITT AAC CAG GTT AAA GAT TCA AAA ATC TCT GCT GAC Lys Lys Val Thr Phe Asn Gln Val Lys Asp Ser Lys Ile Ser Ala Asp 1075
	300	3111012 0112	_ : ( ,		

### **IG.28M**

CAC AAG GIG ACA ( His Lys Val Thr I 1095	AAC ACT GAA GAT ASN Thr Glu ASP 9	GCA AAA AAT GTA ACA ( Ala Lys Asn Val Thr <sup>1</sup> 1125	ATC TCT GCG ACA I Ile Ser Ala Thr 9 1140	ATT AAC GCA ACC ACT (Ile Asn Ala Thr Thr (1155	ATC CTA GGT GGA ATT ( Ile Leu Gly Gly Ile (
ACA CTA CAC AGC AAA GTG GAA ACA TCC GGT AGT AAT Thr Leu His Ser Lys Val Glu Thr Ser Gly Ser Asn 1095	T GAA GAT AGC AGT GAC AAT AAT GCC GGC TTA ACT ATC GAT r Glu Asp Ser Ser Asp Asn Asn Ala Gly Leu Thr Ile Asp 1110	ACA GTA AAC AAT ATT ACT TCT CAC AAA GCA GTG Thr Val Asn Asn Ile Thr Ser His Lys Ala Val 1130	ACA AGT GGA GAA ATT ACC ACT AAA ACA GGT ACA ACC Thr Ser Gly Glu Ile Thr Thr Lys Thr Gly Thr Thr 1145	ACT GGT AAC GTG GAG ATA ACC GCT CAA ACA GGT AGT Thr Gly Asn Val Glu 11e Thr Ala Gln Thr Gly Ser 1160 1160	GGA AITT GAG TCC AGC TCT GGC TCT GTA ACA CTT ACT GCA Gly Ile Glu Ser Ser Ser Gly Ser Val Thr Leu Thr Ala
3668	3716	3764	3812	3860	3908

3956	4004	4052	4100	4148	4196
ACC GAG GGC GCT CTT GCT GTA AGC AAT ATT TCG GGC AAC ACC GTT ACT	GIT ACT GCA AAT AGC GGT GCA TITA ACC ACT TITG GCA GGC TCT ACA ATT	AAA GGA ACC GAG AGT GTA ACC ACT TCA AGT CAA TCA GGC GAT ATC GGC	GGT ACG ATT TCT GGT GGC ACA GTA GAG GTT AAA GCA ACC GAA AGT TTA	ACC ACT CAA TCC AAT TCA AAA ATT AAA GCA ACA ACA GGC GAG GCT AAC	GTA ACA AGT GCA ACA GGT ACA ATT GGT GGT ACG ATT TCC GGT AAT ACG
Thr Glu Gly Ala Leu Ala Val Ser Asn Ile Ser Gly Asn Thr Val Thr	Val Thr Ala Asn Ser Gly Âla Leu Thr Thr Leu Ala Gly Ser Thr Ile	Lys Gly Thr Glu Ser Val Thr Thr Ser Ser Gln Ser Gly Asp Ile Gly	Gly Thr Ile Ser Gly Gly Thr Val Glu Val Lys Ala Thr Glu Ser Leu	Thr Thr Gln Ser Asn Ser Lys Ile Lys Ala Thr Thr Gly Glu Ala Asn	Val Thr Ser Ala Thr Gly Thr Ile Gly Gly Thr Ile Ser Gly Asn Thr
1190	1205	1220	1235	1265	1270

## FIG.28(

4244	4292	4340	4388	4436	4484
GTA AAT GIT ACG GCA AAC GCT GGC GAT TTA ACA GIT GGG AAT GGC GCA 42 Val Asn Val Thr Ala Asn Ala Gly Asp Leu Thr Val Gly Asn Gly Ala 1295	GAA ATT AAT GCG ACA GAA GCA GCT GCA ACC TTA ACT ACA TCA TCG GGC Glu Ile Asn Ala Thr Glu Gly Ala Ala Thr Leu Thr Thr Ser Ser Gly 1300	ASA TTA ACT ACC GAA GCT AGT TCA CAC ATT ACT TCA GCC AAG GGT CAG  Lys Leu Thr Thr Glu Ala Ser Ser His Ile Thr Ser Ala Lys Gly Gln  1315  1320	GTA AAT CTT TCA GCT CAG GAT GGT AGC GTT GCA GGA AGT ATT AAT GCC Val Asn Leu Ser Ala Gln Asp Gly Ser Val Ala Gly Ser Ile Asn Ala 1335	OCC AAT GIG ACA CTA AAT ACT ACA OOC ACT TTA ACT ACC GIG AAG OGT Ala Asn Val Thr Leu Asn Thr Thr Gly Thr Leu Thr Thr Val Lys Gly 1350	TCA AAC ATT AAT GCA ACC AGC GGT ACC TTG GTT ATT AAC GCA AAA GAC Ser Asn Ile Asn Ala Thr Ser Gly Thr Leu Val Ile Asn Ala Lys Asp 1375

	4676	4628	4580	4532
T GAG CTA AAT GGC GCA GCA TTG GGT AAC CAC ACA GTG GTA AAT GCA a Glu Leu Asn Gly Ala Ala Leu Gly Asn His Thr Val Val Asn Ala 1380  1380  2 AAC GCA AAT GCC TCC GGC ACC ACC ACC ACC ACA ACC TCA AGC ACA ACC ACA ACC ACA ACC ATA AAT GCA TCA ATC ACA ATCA AT	AST I LE THE ASA AAC GGT LyS AST GLY AAA TAC ATT LyS TYF I LE LyS TYF I LE	GIG AAC AIC ACT GGG GAT TIA AIC ACA ATA AAT GGA TIA AAT AIC AITT Val Asn Ile Thr Gly Asp Leu Ile Thr Ile Asn Gly Leu Asn Ile Ile 1415	AAT GGC TCC GGC AGC GTA ATC GCG ACA ACC TCA AGC Asn Gly Ser Gly Ser Val Ile Ala Thr Thr Ser Ser 1400	GCA GCA TTG GGT AAC CAC ACA GTG GTA AAT Ala Ala Leu Gly Asn His Thr Val Val Asn 1385

## FIG.280

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AAATATACA AGATAATAAA AATAAATCAA GATTTTTGTG ATGACAAACA ACAATTACAA	09
ACCITITIT GCAGICTATA TGCAAATATT TTAAAAAAT AGTATAAATC CGCCATATAA	120
AIGGIAITAA TCITTICAICT TICAICTITIA AICTITICAIC TITICAICTIT CAICTITICAT	180
THICAICH TCAICHTICA TCHTICAICH TICAICHTIC AICHTICAIC THICAICHT	240
ACATGAAAT GATGAACCGA GGGAAGGGAG GCAGGGGCAA GAATGAAGAG GGAGCTGAAC	300
PACGCAAAT GATAAAGTAA TITAATIGIT CAACTAACCT TAGGAGAAAA T ATG AAC Met Asn 1	357
AG ATA TAT CGT CTC AAA TTC AGC AAA CGC CTG AAT GCT TTG GTT GCT ys ile Tyr Arg Leu Lys Phe Ser Lys Arg Leu Asn Ala Leu Val Ala 5	405
ing ict gaa tiig gea eeg eeg iegt eac ear iec aca gaa aaa eec tiic Val Ser Glu Leu Ala Arg Gly Cys Asp His Ser i'hr Glu Lys Gly Phe 20	453
INC. TAT GIT ACT ATC TIT AGG TGT AAC CAC TTA GCG TTA AAG CCA CTT ANG TYR VAI Thr Ile Phe Ang Cys Asn His Leu Ala Leu Lys Pro Leu 50	501

549	597	645	693	741	789	837
TCC GCT AIG TIA CTA TCT TIA GGT GTA ACA TCT AIT CCA CAA TCT GITT Ser Ala Met Leu Leu Ser Leu Gly Val Thr Ser Ile Pro Gln Ser Val 60 65	TTA GCA AGC GGC TTA CAA GGA ATG GAT GTA GTA CAC GGC ACA GCC ACT Leu Ala Ser Gly Leu Gln Gly Met Asp Val Val His Gly Thr Ala Thr 70	ATG CAA GTA GAT GGT AAT AAA ACC ATT ATC CGC AAC AGT GTT GAC GCT Met Gln Val Asp Gly Asn Lys Thr Ile Ile Arg Asn Ser Val Asp Ala 85	ATC ATT AAT TGG AAA CAA TITT AAC ATC GAC CAA AAT GAA ATG GTG CAG Ile Ile Asn Trp Lys Gln Phe Asn Ile Asp Gln Asn Glu Met Val Gln 100		AAC CAA ATC TCC CAA TTA AAA GGG ATT TTA GAT TCT AAC GGA CAA GTC Asn Gln Ile Ser Gln Leu Lys Gly Ile Leu Asp Ser Asn Gly Gln Val 135	TIT TTA ATC AAC CCA AAT GGT ATC ACA ATA GGT AAA GAC GCA ATT ATT Phe Leu Ile Asn Pro Asn Gly Ile Thr Ile Gly Lys Asp Ala Ile Ile 150
	5	SUBSTITUT	E SHEET (R	IULE 26)		

)		ATC AAG GCG CGT AAT Ile Lys Ala Arg Asn 180	GAA Glu	GTA AAT CTT ATT GGT Val Asn Leu Ile Gly 215	AAT GGT GGC AGC AIT Asn Gly Gly Ser Ile 230		gaa gcc grc aar crc Glu ala Val Asn Leu
	ACG GCT TCT ACG CTA GAC ATT TCT AAC GAA AAC Thr Ala Ser Thr Leu Asp Ile Ser Asn Glu Asn 170	TTC ACC TTC GAG CAA ACC AAA GAT AAA GCG CTC Phe Thr Phe Glu Gln Thr Lys Asp Lys Ala Leu 185	CAC GGT TTA ATT ACT GTC GGT AAA GAC GGC AGT His Gly Leu Ile Thr Val Gly Lys Asp Gly Ser 200	GGC AAA GIG AAA AAC GAG GGT GIG ATT AGC GTA Gly Lys Val Lys Asn Glu Gly Val Ile Ser Val 220	TCT TTA CTC GCA GGG CAA AAA ATC ACC ATC AGC Ser Leu Leu Ala Gly Gln Lys Ile Thr Ile Ser 235	ACC AIT ACT TAC AGC AIT GCC GCG CCT GAA AAT Thr Ile Thr Tyr Ser Ile Ala Ala Pro Glu Asn 255	GOC GAT AIT TIT GCC AAA GOC GGT AAC AITT AAT Gly ASp Ile Phe Ala Lys Gly Gly Asn Ile Asn
	882	933	981	1029	1077	1125	1173

1221	1269	1317	1365	1413	1461	1509
GTC CGT GCT GCC ACT AIT CGA AAC CAA GGT AAA CTT TCT GCT GAT TCT	GTA AGC AAA GAT AAA AGC GGC AAT ATT GTT CTT TCC GCC AAA GAG GGT	GAA GCG GAA AIT GGC GGT GTA AIT TCC GCT CAA AAT CAG CAA GCT AAA	GGC GGC AAG CTG ATG ATT ACA GGC GAT AAA GTC ACA TTA AAA ACA GGT	OCA GIT ATC GAC CIT TCA OGF AAA GAA GOG OGA GAA ACT TAC CIT OOC	GGT GAC GAC GGC GAA GGT AAA AAC GGC ATT CAA TTA GCA AAG AAA	ACC TCT TTA GAA AAA GGC TCA ACC ATC AAT GTA TCA GGC AAA GAA AAA
Val Arg Ala Ala Thr Ile Arg Asn Gln Gly Lys Leu Ser Ala Asp Ser	Val Ser Lys Asp Lys Ser Gly Asn Ile Val Leu Ser Ala Lys Glu Gly	Glu Ala Glu Ile Gly Gly Val Ile Ser Ala Gln Asn Gln Gln Ala Lys	Gly Gly Lys Leu Met Ile Thr Gly Asp Lys Val Thr Leu Lys Thr Gly	Ala Val 11e Asp Leu Ser Gly Lys Glu Gly Gly Glu Thr Tyr Leu Gly	Gly Asp Glu Arg Gly Glu Gly Lys Asn Gly Ile Gln Leu Ala Lys Lys	Thr Ser Leu Glu Lys Gly Ser Thr Ile Asn Val Ser Gly Lys Glu Lys
275	300	310	325	340	355	375

1845

ATG Met

A L

13G 17p

AAC Asn

AAA Lys

CIG

TAT

Ser Ser

AIT Ile

AAT Asn 490

OCC Ala 495

99C 61y TH GAC Asp 400 GGT G1y AIT 11e THA Let 改 GCG Ala AAA Lys ATT 11e gcT Ala GAT ASP 395 99C Gly 13G 17p GIG ATT Ile GGT Gly GCT Ala 390 CGC GGA 99C Gly

# 1557

1605

GIG

G17 415

AAT Asn

AIC Ile

GAT ASP 410 GGT Gly

GAA Glin

AAC Asn

AIT Ile

GCT Ala 405

AGT Ser

206/235

1653

AAA Lys

GIT Val

AIT Ile

9CA Ala

AGC Ser

GAC Asp

AIT 11e

AAT Asn 430

TTA Leu 425 TAT

936 G1y

Set 73

GAG Glu

ACA Thr 420

GAC Asp CAT His

TIG

13G

ACA Thr 435

CTA Leu 440

AAT Asn

ACC

GAG Glu

AAA Lys CCC

CGC Cil

1749

99C G1y

ACA Thr 465

Pro Pro

TIC Phe

GAA Glu

GAT Asp

ATA Ile

GGT GLY

AAT Asn 460

1797

ACG

ACA Ithr

GE CE

GAA Glu

AGC Ser

AAT Asn

AAA Liys 475

AAA Lys

CCT

GAC Asp

AAA Lys 480

1701

GAA Glu 450

gcc Ala

GAA Glu

AIT 11e

ASA Thr

GAT Asp

GAT ASp

Pro Cr

GIA Val 445

AAT Asn 455

Ser Ser GAA Glu

ACC

GGT GLY

Aca Ala 470

ACT ACA Thr AAT Asn 485

CTA

SUBSTITUTE SHEET (RULE 26)

GAC Asp

1893	1941	1989	2037	2085	2133	2181
AAT ATA ACG GCA TCA AGA AAA CTT ACC GIT AAT AGC TCA ATC AAC ATC	GGA AGC AAC TCC CAC TTA ATT CTC CAT AGT AAA GGT CAG CGT GGC GGA	GGC GIT CAG AIT GAT GGA GAT AIT ACT TCT AAA GGC GGA AAT TTA ACC	ATT TAT TCT GGC GGA TGG GTT GAT GTT CAT AAA AAT ATT ACG CTT GAT	CAG GGT TITT TIA AAT ATT ACC GCC GCT TCC GTA GCT TITT GAA GGT GGA	AAT AAC AAA GCA CGC GAC GCA AAT GCT AAA ATT GTC GCC CAG GGC	ACT GTA ACC ATT ACA GGA GAG GGA AAA GAT TTC AGG GCT AAC AAC GTA
Asn ile Thr Ala Ser Arg Lys Leu Thr Val Asn Ser Ser ile Asn ile	Gly Ser Asn Ser His Leu Ile Leu His Ser Lys Gly Gln Arg Gly Gly	Gly Val Gln Ile Asp Gly Asp Ile Thr Ser Lys Gly Gly Asn Leu Thr	Ile Tyr Ser Gly Gly Trp Val Asp Val His Lys Asn Ile Thr Leu Asp	Gln Gly Phe Leu Asn Ile Thr Ala Ala Ser Val Ala Phe Glu Gly Gly	Asn Asn Lys Ala Arg Asp Ala Ala Asn Ala Lys Ile Val Ala Gln Gly	Thr Val Thr Ile Thr Gly Glu Gly Lys Asp Phe Arg Ala Asn Asn Val
500	515	540	550	575	580	595

2229	2277	2325	2373	2421	2469	2517
TCT TTA AAC GGA AGG GGT AAA GGT CTG AAT ATC ATT TCA TCA GTG AAT Ser Leu Asn Gly Thr Gly Lys Gly Leu Asn 11e 11e Ser Ser Val Asn 625	AAT TTA ACC CAC AAT CTT AGT GGC ACA ATT AAC ATA TCT GGG AAT ATA Asn Leu Thr His Asn Leu Ser Gly Thr Ile Asn Ile Ser Gly Asn Ile 630	ACA ATT AAC CAA ACT ACG AGA AAG AAC ACC TCG TAT TGG CAA ACC AGC Thr Ile Asn Gln Thr Thr Arg Lys Asn Thr Ser Tyr Trp Gln Thr Ser 650	CAT GAT TCG CAC TCG AAC GTC AGT CCT CTT AAT CTA GAG ACA CCC CCA His Asp Ser His Trp Asn Val Ser Ala Leu Asn Leu Glu Thr Gly Ala 660	AAT TIT ACC TIT AIT AAA TAC AIT TCA AGC AAT AGC AAA GGC TITA ACA Asn Phe Thr Phe Ile Lys Tyr Ile Ser Ser Asn Ser Lys Gly Leu Thr 675	ACA CAG TAT AGA AGC TCT GCA GGG GTG AAT TTT AAC GGC GTA AAT GGC Thr Gln Tyr Arg Ser Ser Ala Gly Val Asn Phe Asn Gly Val Asn Gly 695	AAC ATG TCA TTC AAT CTC AAA GAA GGA GCG AAA GTT AAT TTC AAA TTA Asn Met Ser Phe Asn Leu Lys Glu Gly Ala Lys Val Asn Phe Lys Leu 710
	_			= 00\		

GGT GGA CAA AAC TCA AGC AGC AGC ATT ACG GGG
Leu Gly Gly Gln Asn Ser Ser Ser Ile Thr Gly 840 845
Glu Liys Ala Ala Asn Val Thr Leu Glu Ala Asn Asn 865 855
ATA AAA CIT GGC AGC Ile Lys Leu Gly Ser 880
GGG AGT TTA AGT TTA ACT GGC GAA AAT GCA GAT ATT Gly Ser Leu Ser Leu Thr Gly Glu Asn Ala Asp Ile 890
CTC ACT ATT TCA GAA AGC GCC ACT TTT AAA GGA AAG ACT AGA Leu Thr Ile Ser Glu Ser Ala Thr Phe Lys Gly Lys Thr Arg 905
CTA AAT ATC ACC GGC AAT TTT ACC AAT AAT GGC ACT GCC GAA Leu Asn ile Thr Gly Asn Phe Thr Asn Asn Gly Thr Ala Glu 920
ATA ACA CAA GGA GTG GTA AAA CTT GGC AAT GTT ACC AAT GAT Ile Thr Gln Gly Val Val Iys Leu Gly Asn Val Thr Asn Asp 935

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3237	3285	3333	3381	3429	3477	3525
GGT GAT TTA AAC ATT ACC ACT CAC GCT AAA CGC AAC CAA AGA AGC ATC	ATC GGC GGA GAT ATA ATC AAC AAA AAA GGA AGC TTA AAT ATT ACA GAC	AGT AAT AAT GAT GCT GAA ATC CAA ATT GGC GGC AAT ATC TCG CAA AAA	GAA GGC AAC CTC ACG ATT TCT TCC GAT AAA ATT AAT ATC ACC AAA CAG	ATA ACA ATC AAA AAG GGT AIT GAT GGA GAG GAC TCT AGT TCA GAT GCG	ACA AGT AAT GCC AAC CTA ACT ATT AAA ACC AAA GAA TTG AAA TTG ACA	GAA GAC CTA AGT ATT TCA GGT TTC AAT AAA GCA GAG ATT ACA GCC AAA
Gly Asp Leu Asn Ile Thr Thr His Ala Lys Arg Asn Gln Arg Ser Ile	Ile Gly Gly Asp Ile Ile Asn Lys Lys Gly Ser Leu Asn Ile Thr Asp	Ser Asn Asn Asp Ala Glu Ile Gln Ile Gly Gly Asn Ile Ser Gln Lys	Glu Gly Asn Leu Thr Ile Ser Ser Asp Lys Ile Asn Ile Thr Lys Gln	Ille Thr Ile Lys Lys Gly Ile Asp Gly Glu Asp Ser Ser Ser Asp Ala	Thr Ser Asn Ala Asn Leu Thr Ile Lys Thr Lys Glu Leu Lys Leu Thr	Glu Asp Leu Ser Ile Ser Gly Phe Asn Lys Ala Glu Ile Thr Ala Lys
950	970	980	995	1015	1030	1045

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3573	3621	3669	3717	3765	3813	3861
GAT GGT AGA GAT TTA ACT ATT GGC AAC AGT AAT GAC GGT AAC AGC GGT. Asp Gly Arg Asp Leu Thr Ile Gly Asn Ser Asn Asp Gly Asn Ser Gly 1060	GCC GAA GCC AAA ACA GTA ACT TIT AAC AAT GTT AAA GAT TCA AAA ATC	TCT GCT GAC GGT CAC AAT GTG ACA CTA AAT AGC AAA GTG AAA ACA TCT	AGC AGC AAT GGC GGA CGT GAA AGC AAT AGC GAC AAC GAT ACC GGC TTA	ACT ATT ACT GCA AAA AAT GTA GAA GTA AAC AAA GAT ATT ACT TCT CTC	AAA ACA GTA AAT ATC ACC GCG TCG GAA AAG GTT ACC ACC ACA GCA GCC	TCG ACC ATT AAC GCA ACA AAT GGC AAA GCA AGT ATT ACA ACC AAA ACA
	Ala Glu Ala Lys Thr Val Thr Phe Asn Asn Val Lys Asp Ser Lys Ile	Ser Ala Asp Gly His Asn Val Thr Leu Asn Ser Lys Val Lys Thr Ser	Ser Ser Asn Gly Gly Arg Glu Ser Asn Ser Asp Asn Asp Thr Gly Leu	Thr 11e Thr Ala Lys Asn Val Glu Val Asn Lys Asp 11e Thr Ser Leu	Lys Thr Val Asn Ile Thr Ala Ser Glu Lys Val Thr Thr Thr Ala Gly	Ser Thr Ile Asn Ala Thr Asn Gly Lys Ala Ser Ile Thr Thr Lys Thr
	1075	1095	1110	1125	1140	1155

3909	3957	4005	4053	4101	4149	4197
GGT GAT ATC AGC GGT ACG ATT TCC GGT AAC ACG GTA AGT GTT AGC GCG Gly Asp Ile Ser Gly Thr Ile Ser Gly Asn Thr Val Ser Val Ser Ala 1175	ACT GGT GAT TTA ACC ACT AAA TCC GGC TCA AAA ATT GAA GCG AAA TCG Thr Gly Asp Leu Thr Thr Lys Ser Gly Ser Lys Ile Glu Ala Lys Ser 1190	GGT GAG GCT AAT GTA ACA AGT GCA ACA GGT ACA ATT GGC GGT ACA ATT GLY Gly Gly Gly Thr Ile Gly Gly Thr Ile Gly Gly Thr Ile 1205	TCC GGT AAT ACG GTA AAT GTT ACG GCA AAC GCT GGC GAT TTA ACA GTT Ser Gly Asn Thr Val Asn Val Thr Ala Asn Ala Gly Asp Leu Thr Val 1220	GGS AAT GGC GCA GAA AIT AAT GCG ACA GAA GGA GCT GCA ACC TIA ACC GIY Asn Gly Asn Gly Ala Glu Ile Asn Ala Thr Glu Gly Ala Ala Thr Leu Thr 1235	GCA ACA GGG AAT ACC TIG ACT ACT GAA GCC GGT TCT AGC ATC ACT TCA Ala Thr Gly Asn Thr Leu Thr Thr Glu Ala Gly Ser Ser Ile Thr Ser 1265	ACT AAG GGT CAG GTA GAC CTC TTG GCT CAG AAT GGT AGC ATC GCA GGA Thr Lys Gly Gln Val Asp Leu Leu Ala Gln Asn Gly Ser Ile Ala Gly 1270

4245	4293	4341	4389	4437	4485	4533
AGC AIT AAT GCT AAT GIG ACA TTA AAT ACT ACA GGC ACC TTA ACC Ser Ile Asn Ala Ala Asn Val Thr Leu Asn Thr Thr Gly Thr Leu Thr 1295		AAC GCA AAA GAT ÖCT AAG CTA AAT GGT GAT GCA TCA GGT GAT AGT ACA Asn Ala Lys Asp Ala Lys Leu Asn Gly Asp Ala Ser Gly Asp Ser Thr 1315			TTA AAT ATC ATT TCG AAA GAT GGT AGA AAC ACT GTG CGC TTA AGA GGC Leu Asn Ile Ile Ser Lys Asp Gly Arg Asn Thr Val Arg Leu Arg Gly 1365	AAG GAA ATT GAG GTG AAA TAT ATC CAG CCA GGT GTA GCA AGT GTA GAA Lys Glu Ile Glu Val Lys Tyr Ile Gln Pro Gly Val Ala Ser Val Glu 1380

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FIG.30A	Alignment	of HMW pro	teins	
10 MNKIYRLKFSKRI		30 RGCDHSTEKGSI	40 EKPARMKVRH	50 LALKPLSAMILS
110 NWKQFNIDQNEM	120 VQFLQENNNSAV	130 /FNRVTSNQIS	140 QLKGILDSNG	150 QVFLINPNGITI
210 GLITVGKDGSVN	220 LIGGKVKNEGV			
		330 GKLMITGDKVI		350 GKEGGETYLGGD
GNINAQGSGDIA	420 KTGGFVETSGH	DLFIKDNAIVI	AKEWILLDPDA TTI	450 WSINAETAGRSN D.T.EDPL.NT.E.PSYS.GYGDDG.SE.NDENPSTE.ND E.T.G.GDVD DD.PS.E.TDN.VKG.ELQND D.T.A.GAPNDPALTE DIN.WVGSNIDAQ
.SRKLT .KKNLT .NE.RD. .RKTD. .TDN	NL-SNGSLTLW .IGSH.I.H .IGDSSH.I.H .IGG.SH .IKDSSH.I	.K.QRQ KNNK .SKNKNSL NDNSSC GGNK	INNDITTGDD .DGSKESGNSKGNS	550 TRGANLTIYSGGWK.GQN.GQANGST.GSST.GSN.KAT.GSV.S

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### FIG.30B

60	70	80	90	100	
LGVTSIPQ	SVLASGLQGM	DVVHGTATMQ	VDGNKTIIR	NSVDAII	12-1
					12-2
160	170	180	190	200	
	170 NGFTASTLDI				12-1
	IMPLIADITEDT				12-1
• • • • • • •	• • • • • • • • •		• • • • • • • •	•••••	12-2
260	270	280	290	300	
ENEAVNLG	DIFAKGGNIN	VRAATIRNQG	KLSADSVSK	DKSGNIV	12-1
				• • • • • •	12-2
360	370	300	390	400	
	370 HOLAKKTSLE				12-1
	TÄTHVVISTE				12-1
• • • • • • •	• • • • • • • • •	• • • • • • • • •		• • • • • •	12-2
460	470	480	49	0 500	
TS-EDDEY	-TGSGNSAST	PKRNKEKT	TLINITLES	ILKKGTFV-NIT	12-1
.G-INF	PTGED	K.S.L	ISN	YNAWIM	12-2
AG-I.S.F	PGTKE	T.G.Q-P.	VE.ISN	YSW.M	15-1
.NL.NE	T.ED.	$\dots$ NNT- $\dots$	SK	AR.S	15-2
APTEDF	P.A.GKDN-	K.AHNF	)IF	RSGN	Joyc-1
SNL	T.ENINN	V. <b>N</b> QSK	SSIN	IS	Joyc-2
DS.TAF	PT.ERN	T.AQN-RE	P.ISQ	)N	LCDC2-
.GV	T.ADINH	Q.Q.S.TS	5	MR.L	LCDC2-
LV-V	<u>R.D</u> I	E.K.APT	.IHAGSI.Q	QS.MGAS	PMH1-1
GVFF	P. <u>R.D</u> D. N	A.T.HPDE	1.V	IANN	PMH1-2
STPNNN	-D.P.QINY	KPS-LS	5 F	RRN.S	K1-1
LQP	<u>R.D</u>	.NKVSAEGL.	SIN.AST	TA.QIES	K21-1
560	570	580		590	
	SLGAQGNINIT		(GS-N		12-1
	r.dFL				12-2
	rTTL				15-1
	Γ.ESRL			· ·	15-2
	r.NSLL				Joyc-1
				AADAQ.VA.	-

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### FIG.30C

.RNK.RI	IGDS.H.	YKKRKNI	RSD.IQK.	SG.S-	$\dots$ N.DD.
.TNKVN.TTI	)V-YA.	HRD	GN	S <b>EKN</b> G.	KA.S.
				STNG.	
				STNG.	
				SQNG.	
				~	
		610		63	
GTITSGNQ	Q-KGFRFNN	/SLNGTGSGI	LQFTTKRTN-	KYAITN	KFEGTLNI
.TVGEG-	DA	K.	.NIISSVN	L.H	NLSI
NIGI	Q.QL.L	.II.	.N.VSIQP	TSH	R.D.E.I.
				KNINSLV	
				GNNFQ.I.	
				Q.Н	
ASK-	D.	.T.S.VKK.	FL.KYSQ	NNKDSNFE.	H.R
LTGE	EN.TL	N.	.SIISTAS	LSH	RLD.EI.V
NNKI	G.QL.L.	A.	.N.IANQN		NIS.AI
VVC	G-E	V.A.	.R.VGQKNIS	SNSWRENT.K.	R.D.N
2\1\1\1\1	z_ n	.TG.	.S.KYIE.G-	NRDSNFE.H	IR.R
· · · · · · · · · · · · · · · · · · ·	· · · · · · · · · · · · · · · · · · ·				
					ID
				Н.Н	ID
	EN.QLS.	M.A.	.TANKG		
N.I.NQI	EN.QLS. 690	M.A.	.TANKG 710	Н.Н	730
N.I.NQI	EN.QLS. 690 -DSAGTLTQI	M.A. 700 PYNLNGISF	.TANKG 710 NKDTTFNVER	н.н 720	730 PIG-INKYS
N.I.NQI DSRGS SNSKGI	EN.QLS. 690 -DSAGTLTQI LTTQYRSSA	M.A. 700 PYNLNGISF .V.FVNG	.TANKG 710 NKDTTFNVER .M-SLKE	H.H 720 NARVNFDIKAF	730 PIG-INKYS NE-NMNT.
N.I.NQI DSRGS SNSKGI LNNNH-GRET	EN.QLS. 690 -DSAGTLTQI LTTQYRSSA ISR-YRKGG	M.A. 700 PYNLNGISF .V.FVNG GVIFRSPIG	.TANKG 710 NKDTTFNVER .M-SLKE HTNT.KQ	H.H 720 NARVNFDIKAF G.KKL	730 PIG-INKYS NE-NMNT. ND-T.HAN
DSRGSSNSKGI	EN.QLS.  690  -DSAGTLTQI LTTQYRSSA ISR-YRKGG E.GSAP.LS	700 PYNLNGISF V.FVNG GVIFRSPIG	.TANKG 710  NKDTTFNVER .M-SLKE HTNT.KQ	H.H 720 NARVNFDIKAF G.KKL GSVASFK	730 PIG-INKYS NE-NMNT. ND-T.HAN TQ.N
DSRGSSAI	EN.QLS.  690  -DSAGTLTQI LTTQYRSSA ISR-YRKGGGE.GSAP.LSITNT	700 PYNLNGISF V.FVNG GVIFRSPIG S.T	.TANKG 710  NKDTTFNVER .M-SLKE HTNT.KQ TTNK	H.H 720 NARVNFDIKAF G.KKL GSVASFK	730 PIG-INKYS NE-NMNT. IND-T.HANT.Q.N
DSRGSSNSKGI LNNNH-GRETSAID	EN.QLS.  690  -DSAGTLTQI LTTQYRSSA ISR-YRKGG E.GSAP.LSITNT PLRSSG	700 PYNLNGISF V.FVNG GVIFRSPIG S.T GVFFING	TANKG 710  NKDTTFNVER .M-SLKE HTNT.KQ TTNKI.D.KQ	720  NARVNFDIKAF G.KKL GSVASFKKN	730 PIG-INKYS NE-NMNT. ND-T.HANT.Q.NV.NNR .NE-NT.N.
DSRGSSNSKGI LNNNH-GRETSAID E.NRFGPTTI	EN.QLS.  690  -DSAGTLTQI LTTQYRSSA ISR-YRKGG E.GSAP.LSTNT PLRSSG SPGP.YR	700 PYNLNGISF V.FVNG GVIFRSPIG S.T GVFFING	TANKG 710  NKDTTFNVER .M-SLKE HTNT.KQ TTNKI.D.KQ	720  NARVNFDIKAF G.KKL GSVASFKKN	730 PIG-INKYS NE-NMNT. IND-T.HANT.Q.NV.NNR .NE-NT.N.
DSRGS SNSKGI LNNNH-GRETSAID E.NRFGPTTI .NS.SRPS	EN.QLS.  690  -DSAGTLTQI LTTQYRSSA ISR-YRKGG E.GSAP.LSTNT PLRSSG SPGP.YRGRSFA	700 PYNLNGISF V.FVNG GVIFRSPIG S.T GVFFING RSG	TANKG 710  NKDTTFNVER .M-SLKE HTNT.KQ TTNKI.D.KQ .MVLGT .N.VAS	720 NARVNFDIKAF G.KKL GSVASFKKN O.GA.T GSASP.	730 PIG-INKYS NE-NMNT. TND-T.HANTQ.NV.NNR .NE-NT.NV-S.VHD
DSRGSSKGI LNNNH-GRETSAID E.NRFGPITI .NS.SRPS N.ARNGDVRNHSTI	EN.QLS.  690  -DSAGTLTQI LTTQYRSSA ISR-YRKGG E.GSAP.LSTNT PLRSSG SPGP.YRGRSFA NSSDSRSFA	700 PYNLNGISF V.FVNG GVIFRSPIG S.T GVFFING RSG GVIF.AKGL	T. ANKG 710  NKDTTFNVER .M-SLKE HTNT.KQ TTNKI.D.KQ .MVLGT .N.VAS .TTSKK	720  NARVNFDIKAF G.KKL GSVASFK KN  O.GA.T  CSSASP.  GST.D.KL	730 PIG-INKYS NE-NMNT. IND-T.HANTQ.NV.NNR .NE-NT.NV-S.VHD .NSGYNSQK
DSRGS SNSKGI LNNNH-GRETSAID E.NRFGPTTI .NS.SRPS N.ARNGDVRNHSTI .AS.ISSGW	EN.QLS.  690  -DSAGTLTQI LTTQYRSSA ISR-YRKGG E.GSAP.LSTNT PLRSSG SPGP.YRGRSFA NSSDSRSFA	700 PYNLNGISF V.FVNG GVIFRSPIG S.T GVFFING RSG GVIF.AKGL GVKFH.KNN	T. ANKG 710  NKDTTFNVER .M-SLKE HTNT.KQ TTNKI.D.KQ .MVLGT .N.VAS .TTSKK EMKIGN	720  NARVNFDIKAF G.KKL GSVASFKKN C.GA.T GSASP. GST.D.KL IKAE.RL	730 PIG-INKYS NE-NMNT. AND-T.HANTQ.NV.NNR .NE-NT.NV-S.VHD .NSGYNSQK .NEKTTPNR .SVMTP.PN.
DSRGS SNSKGI LNNNH-GRETSAID E.NRFGPTTI .NS.SRPS N.ARNGDVRNHSTI .AS.ISSGW	EN.QLS.  690  -DSAGTLTQI LTTQYRSSA ISR-YRKGG E.GSAP.LSTNT PLRSSG SPGP.YRGRSFA NSSDSRSFA	700 PYNLNGISF V.FVNG GVIFRSPIG S.T GVFFING RSG GVIF.AKGL GVKFH.KNN	T. ANKG 710  NKDTTFNVER .M-SLKE HTNT.KQ TTNKI.D.KQ .MVLGT .N.VAS .TTSKK EMKIGN	720  NARVNFDIKAF G.KKL GSVASFK  G.GA.T  GSAS.P.  GST.D.KL  J.KAE.RL  GSTAHTS	730 PIG-INKYS NE-NMNT. AND-T.HANTQ.NV.NNR .NE-NT.NV-S.VHD .NSGYNSQK .NEKTTPNR .SVMTP.PN.
DSRGS SNSKGI LNNNH-GRETSAID E.NRFGPTTI .NS.SRPS N.ARNGDVRNHSTI .AS.ISSGNSGSAS	EN.QLS.  690  -DSAGTLTQI LTTQYRSSA ISR-YRKGG E.GSAP.LSTNT PLRSSG SPGP.YRGRSFA NSSDSRSFA QDDITNRG- SPGP.NA	700 PYNLNGISF V.FVNG GVIFRSPIG S.T GVFFING RSG GVIF.AKGL GVKFH.KNNT. QSG	T. ANKG  710  NKDTTFNVER .M-SLKE HTNT.KQ TTNKI.D.KQ .MVLGT .N.VAS .TTSKK EMKIGN .GENIAQ	720  NARVNFDIKAF G.KKL GSVASFK  G.GA.T  GSAS.P.  GST.D.KL  J.KAE.RL  GSTAHTS	730 PIG-INKYS NE-NMNT. IND-T.HANTQ.NV.NNR .NE-NT.NV-S.VHD .NSGYNSQK .NEKTTPNR SVMTP.PN.
DSRGS SNSKGI LNNNH-GRETSAID E.NRFGPTTI .NS.SRPS N.ARNGDVRNHSTI .AS.ISSGNSGSAS	EN.QLS.  690  -DSAGTLTQI LTTQYRSSA ISR-YRKGG E.GSAP.LSTNT PLRSSG SPGP.YRGRSFA NSSDSRSFA QDDITNRG- SPGP.NA	700 PYNLNGISF V.FVNG GVIFRSPIG S.T GVFFING RSG GVIF.AKGL GVKFH.KNNT. QSG	T. ANKG  710  NKDTTFNVER .M-SLKE HTNT.KQ TTNKI.D.KQ .MVLGT .N.VAS .TTSKK EMKIGN .GENIAQ	720  NARVNFDIKAF  G.KKL  GSVASFK  C.SL.NL  GSAS.P.  GST.D.KL  XGST.D.KL  XGSTAHTS	730 PIG-INKYS NE-NMNT. IND-T.HANTQ.NV.NNR .NE-NT.NV-S.VHD .NSGYNSQK .NEKTTPNR SVMTP.PN.
DSRGS SNSKGI LNNNH-GRETSAID E.NRFGPTTI .NS.SRPS N.ARNGDVRNHSTI .AS.ISSGNSGSAS	EN.QLS.  690  -DSAGTLTQI LTTQYRSSA ISR-YRKGG E.GSAP.LSTNT PLRSSG SPGP.YRGRSFA NSSDSRSFA QDDITNRG- SPGP.NA	700 PYNLNGISF V.FVNG GVIFRSPIG S.T GVFFING RSG GVKFH.KNNT. QSG	T. ANKG  710  NKDTTFNVER .M-SLKE HTNT.KQ TTNKI.D.KQ .MVLGT .N.VAS .TTSKK .EMKIGN .GENIAQ	720  NARVNFDIKAF  G.KKL  GSVASFK  C.SL.NL  GSAS.P.  GST.D.KL  XGST.D.KL  XGSTAHTS	730 PIG-INKYS NE-NMNT. AND-T.HANT.Q.NV.NNR .NE-NT.NV-S.VHD .NSGYNSQK .NEKTTPNR SVMTP.PNV-DKVIN
DSRGS SNSKGI LNINH-GRETSAID E.NRFGPTTI .NS.SRPS N.ARNGDVRNHSTI .AS.ISSGNSGSASNRSVA 79 RFKTSGSTK	EN.QLS.  690  -DSAGTLTQI LTTQYRSSA ISR-YRKGG E.GSAP.LSTNT PLRSSG SPGP.YRGRSFA NSSDSRSFA QDDITNRG- SPGP.NA LNSGSRSFA  0 8 TGFSIEKDL	700 PYNLNGISF V.FVNG SVIFRSPIG S.T GVFFING RSG GVKFH.KNNT. QSG GVKFY.KNN	T. ANKG  710  NKDTTFNVER .M-SLKE HTNT.KQ TTNKI.D.KQ .N.V.AS .MVLGT .N.V.AS .TTSKK .GEN.IAQ .N.V.IAA	720 NARVNFDIKAF G.KKL GSVASFKKN C.GA.T C.SL.NL GSSAS.P. GST.D.KL XGSTAHTS ASSANP. 820 -DEMIGK-GIVE	730 PIG-INKYS NE-NMNT. NID-T.HANT.Q.NV.NNR .NE-NT.NV-S.VHD .NSGYNSQK .NEKTTPNR EVMTP.PNV-DKVIN NDNTSNNKP 830 AKKNITFEG
DSRGS SNSKGI LNINH-GRETSAID E.NRFGPTTI .NS.SRPS N.ARNGDVRNHSTI .AS.ISSGNSGSASNRSVA 79 RFKTSGSTK	EN.QLS.  690  -DSAGTLTQI LTTQYRSSA ISR-YRKGG E.GSAP.LSTNT PLRSSG SPGP.YRGRSFA NSSDSRSFA QDDITNRG- SPGP.NA LNSGSRSFA  0 8 TGFSIEKDL	700 PYNLNGISF V.FVNG SVIFRSPIG S.T GVFFING RSG GVKFH.KNNT. QSG GVKFY.KNN	T. ANKG  710  NKDTTFNVER .M-SLKE HTNT.KQ TTNKI.D.KQ .N.V.AS .MVLGT .N.V.AS .TTSKK .GEN.IAQ .N.V.IAA	720 NARVNFDIKAF G.KKL GSVASFK C.KN C.GA.T C.SASP. C.ST.D.KL C.STAHTS ASSANP. 820	730 PIG-INKYS NE-NMNT. NID-T.HANT.Q.NV.NNR .NE-NT.NV-S.VHD .NSGYNSQK .NEKTTPNR EVMTP.PNV-DKVIN NDNTSNNKP 830 AKKNITFEG

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### FIG.30D

T.NSYLI.GTEFLT.NTYLT.KSYLT.MFL.	SSD-SV. SG GG-SV. TG	G.NG.KGR N AGNEKGR DKPGLS	SSASAQ.IA LTA QVSESKA NLTA	K	LCDC2-1 LCDC2-2 PMH1-1 PMH1-2 K1-1 K21-1
640 650  SGKVNISMVLPKNESG .NIT.NQTTRTR.HVNQTTLS. IP.NAT.NIKWD T.N.T.NQTA.ATTAD.L.QARQENWN .N.T.NQTTQQ.IEV.T.NQTK.AKV.DVSGTKWHD.L.QARQENWNV.NQTT.HIA	WQTSHDSI -FW.VSDES W.SRYSRWN.SYDS I-RRHSSW.ASSDSAWNTSYDS I-TRIN I-RRHWS	HVSALEVSH.T.KI.HAVSTQ HV.RVST.TLVST.TL.	ESGEFNLT- TGAN.TFIK .KSA.SF.K .DSNGSKKNSS.TFIK TNSYL.I R.DSK.TFIK NDAK.TFIK NDAK.TFIK	Y. FA  RT  YV YV 	12-1 12-2 15-1 15-2 Joyc-1 Joyc-2 LCDC2-1 LCDC2-2 PMH1-1 PMH1-2 K1-1 K21-1
740 SLNYASFNGNISVSCO KPLPIR.LA. TATQLPIQ.SD. NL. N. KP.PLQ. A. TAI. GHTLVL. RIPIQ.QS. PLPIQ.LSTLL. GHTL.KL.	GSVDFTLLAF.DIYK.L.CITS .N.T.R.NN.T.K S.DIHD.N.HFNR.NINTNF.DIY.N .T.N.E.N	NHGR. A  NYGRS Q  TA  NHGR. A HW. H.  ILTGG!  ILWGK. TI THT. S. A	VINSKYFNVAELKMSEI.I G.GMSSI IHL.A FH.A AELKMNTI.I L.K.QN.A E.R.SSI.A ELKMDSI.A IQN	STGSSL I.N.ANF .DN. A.K A.G I.D.T A.E DTSNGK.	12-1 12-2 15-1 15-2 Joyc-1 Joyc-2 LCDC2-1 LCDC2-2 PMH1-1 PMH1-2 K1-1 K1-1
840 89 GNITFGSRKAVTEIE	GNVTININAI	=			12-1

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### FIG.30E

T.NS.IRGQEA.N.SISFFE.G.YSD.FNGNGFNHDA.KSTHSIL.
E.TVL.NNSIEVT.
E.RAEVL.NNSIVA.
TLOSHVRKDSA.I.SIS.FE.SPDSFT.KYP.R-A.SSTIS.
SER.A.TSS.NA.INLQSLN
SMTAQARDRNA.E.TVISNS.LSII.QNDGFDNNQKAN-A.NS.Y.V.IQ.
TLNSHVRKYNA.E.NINS.FN.R.TSDSFRN.YRNN-A.NSTHSIL.
NL.AN.A.L.KNNEIKSR.QVEQI
K.SE.HAA.T.KN.I.S.N.A.ISNLKSLI.N
SINSHVRGNNA.E.KIIS.FN.K.TKDKFDNSYEKN-A.FSTH.L.IL.
890 900 910 920 930
INSCNLTAGGNIVNIAGNLTVESNANFKAITNFTFNVGGLFDNKGNSNISIAKGGA
LVN.S.SLT.ENAD.KISES.TGK.RD.L.IT.N.T.N.TAE.N.TQ.VV
.ESLI.ASANS.KEKGE.QDNL.IT.T.I.N.D.K.N.SQ.VV
NRNGLN
V-ELT.SVAD.KSILND.TGE.SENL.IT.N.T.N.TAD.N.KQ.VV
KVT.SAIEKGS.K.L.NP.YSSQ.K
VEE.RLV.ASANNS.K.G.KEDNL.IT.T.T.N.T.I.DVKA.
VESLI.ENANSI.KE.IGK.KDSL.IT.N.T.N.TAE.N.SQ.VV
TAND.DTIK.KD.AQG.K.NGS.KNNL.IT.T.T.N.T.I.D.TQ.VV
NKVT.SAIEKGS.K.L.NP.YSSQ.K
SVGNII.SNAH.DSIAES.K.QGKNNL.IT.T.T.N.TAD.N.KQ.VV
990 1000 1010 1020 1030
TEMQIGGDVSQKEGNLTISSDKINITKQITIKAGVDGENSDSDATNNANLTIKTKE
A.INIK.ID.SS
A.INI
A.INIKNSTKSQ
A.ININK.NK.DSTA
A.INIKKECGSPAST
A.ININKNK.DSTA
INI
A.IENI
A.IENI
.INIVERN.DNEATS
A.INI

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### FIG.30F

.V.L.GQNSSSS.T. I. EKA. EANNAP.Q.NIRDRV.LG-SL .V.L.GQDSSST.T.IN.SQA. RAYNGNGRNQLGN.SK.I.K.E.T.A. ND.KN.GVK.I.AVSL.GQNSSSD.K.I.KSST. KAHNSPRDFASRTLGNLNLAAD.KPI.K.I.VKEG. RSANYG.DKSA.S.R-GN.T .V.L.GQNSSST.T.S.N.GA. QAHNGNDRNKFGN.S .V.L.GQNSSSS.M. II.KRA. EADNSH.SDNV.DR.NLGNLTL.Q.P.K.D.VKQGT.A.RSANGAL.VNGNLAAD.KPI.K.I.VKEG. RSANYG.DKSA.SRGN.T .V.L.GENSSSN.K.IN.SK. QAHAGTS.LDK.ER.LTLGN	12-2 15-1 15-2 Joyc-1 Joyc-2 LCDC2-1 LCDC2-2 PMH1-1 PMH1-2 K1-1 K21-1
940 950 960 970 980	12-1
RFK-DIDNSKNLSITTNSSSTYRTIISGNITNKNGDLNITNEGSD	
KLG-NVT.DGD.NHAKRNQ.SG.D.IK.SDSNN.	12-2
KLG-NVT.DGD.NHAKHNQ.SG.D.IK.SDSNKN	15-1 15-2
KN.TSS.NDTEAIDNKGN	
K N. TSS. N DT	Joyc-1 Joyc-2
NIQGN.T.KGG.NAQNNQKNEGKDSNNN HN.T.S.ND.AESDNKNN	LCDC2-1
	LCDC2-2
KLG-N.T.DGNAKNGQKSV.NNK.AN.N. SLGT.DGK.NHAK.GQKS <u>R.D</u> .IQ.NDNN.N	PMH1-1
	PMH1-2
NLG-NVT.DGK.NHAK.GQKS <u>R.D</u> .IQ.NDNN.N	K1-1
IE.TGS.NK.D.NHHKRKN.DN	K1-1 K21-1
KLQGT.NGNA.VNQKNKDIKAN	V∑1_1
1040 1050 1060 1070 1080	
LKLTODLNISGFNKAEITAKDGSDLTIGNIN-SADGINAKKVIFN	12-1
E.SRS.DGNS.AE.T	12-2
	15-1
K.VS.NSDD.GNST	15-2
.QGDE.AISDNNNNA	Joyc-1
.EG	Joyc-2
.QGDE.AISDNNNA	LCDC2-1
ENDVENNN.ING.NAT	LCDC2-2
.TDNNIKAS.NSQD	PMH1-1
.TF.DN	PMH1-2

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### FIG.30G

	1090	1100	1110	1120	1130
N N K N K		. N K. – . S	GGR.SN VIDG.G.G.G. VIDGG GDA.SNIVGI DSSADN GDA.SNIVGI G.SGN DGS.GNGI DGS.GNGI	NA-GLTIDAKN DTTATTD .ST-SNTSD .CT-SNNISD .NISD	EKD E.K D.E D.E D DV I D D D D
1190 SVTLTA	1200 ATEGALAVSI			STI	
N.NI.	.SGDT.N GE	A T.QNA	AVTK.  .K.KQ	NATTGSANI	TTKTGEING
	.SGDT.N		AVTK.	NATTCIVAN	ITTKTGEING
NATIG	DANITTQTC		SVTLIATGQI	  LAVGNISGDIV	  TITADKGKLT 
	DVNITTSTO	GSINGKIESKS	GSVTLTATEKT	LIVGNVSGNIV	TVTANRGALT

### FIG.30H

NN.NDNSDGN.DS .TDNNIKAS.NSQID	K1-1 K21-1
1140       1150       1160       1170       1180         HKAVSISATSGEITTKTGTTINATTGNVEITAQIGSILGGIESSSG       L.T.N.T.SEK-V. TA.S. N.KAS. TK. D.S       N.KAS. TK. D.S         N.T.N.T.SEK-L. ADA. V. K. D.K. EVK.T       V. K. D.K. EVK.T         .T.N.T.SEN-V. A. I.S. V. K. D.K. N.       V. K. D.K. N.         .T.N.T.SEN-V. A. S. V. K. D.S       V. K. D.K. KV. T.         .T.N.T.SERD. AD. KL. V.SD K.N.       V. K         .T.N. SE.G. A. S. V. K       S. V. K         .T.N. SE.G. A. S. V. K. D.K. N.       S. V. K. D.K. N.         .T.N. SE.G. A. S. V. K. D.K. N.       S. V. K. D.S.T. SGKTV	12-1 12-2 15-1 15-2 Joyc-1 Joyc-2 LCDC2-1 LCDC2-2 PMH1-1 PMH1-2 K1-1 K21-1
EVKSASGNVNITASGNTLNVSNITGQNVTVTANSGAITTTEGSTI  EVKSASGNVNITASGNTLNVSNITGQNVTVTANSGAITTTEGSTI	12-1 12-2 15-1 15-2 Joyc-1 Joyc-2 LCDC2-1 LCDC2-2 PMH1-1 PMH1-2 K1-1 K21-1
1220 1230 1240 1250	12-1 12-2 15-1 15-2 Joyc-1 Joyc-2

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FIG.30I
114.001
NATTGDANITTQTGNINGKVESSSGSVTLIATGQTLAVGNISGDTVTTTADKGKLT
TDLTTVKGGAKINATEGTATLTASSGKLT
TTQADSKIEATEGEANVTSKTSIIGGTISGGTVEVTATEGLTTQAGSTITGTESVT
1260 1270 1280 1290 1300
<del></del>
TTQSNSKIKATTGEANVTSATGTIGGTISGNIVNVTANAGDLIVGNGAEINATEGA
K.GE.KS
ITLNVSVSGN.
I.K.G.EAVDTEDA.K.DG
AGE.KTDNIKDR.KG
K.G.EKATEDA.K.DG
KGKT
RKA.T.S
RKA.T.S
AGE.KTDNIKDR.KG
GD.K
1360 1370 1380 1390 1400
1300 20.0
LNITGILTIVKGSNINATSGILVINAKDAELNGAALGNHIVVNATNANGSGSVIAT
AD.KKD.S.DS.EVST.A
EAKS.DST.V
ASNE.S

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### FIG.30J

SAING.ASNK.S.I-GD. TLAGSTIN.NGEEVT.K.S.T.AG	LCDC2-1 LCDC2-2 PMH1-1 PMH1-2
TQTSSKINKSNS.SG TEANSAIS.ANGASKS.T.SSG	K1-1 K21-1
TSSQSGNIGGMISGGKVEVSATKDL	12-1 12-2 15-1 15-2
	Joyc-1 Joyc-2 LCDC2-1 LCDC2-2 PMH1-1
	PMH1-1 PMH1-2 K1-1 K21-1
1310 1320 1330 1340 1350 ATLITSSGKLTTEASSHITSAKGQVNLSAQDGSVAGSINAANVT . ATGNT . G.S. T D.L . N . I	12-1 12-2 15-1 15-2 Joyc-1 Joyc-2 LCDC2-1 LCDC2-2 PMH1-1 PMH1-2 K1-1 K21-1
1410 1420 1430 1440 1450 TSSRVNITGDLITINGLNIISKNGINIVLLKGVKIDVKYIQPGIS. N.V. D.R. R.R.KE.EVN. S.V. R. V. TE.EV	12-1 12-2 15-1

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### FIG.30K

AS	.N	E.S.		
ES				
EE				
EE				
AK.E				
I				
• • • • • •	· · · · · · · · · · · · · · · · · · ·	2	511.5	
1460	1470	1480 1	.490	1500
ASVDEVIEAKRILEK	/KDLSDEEREA	LAKLGVSAVRF	'IEPNNTIT'	/DIQNEFATRP
EV	Т		V	.N
EV	т			.N
			AA]	INT
YA				
ANA	Т		VV	NT
EV				
EV				
EV				
NA				
ANA				
	<del>.</del>			

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## FIG.30L

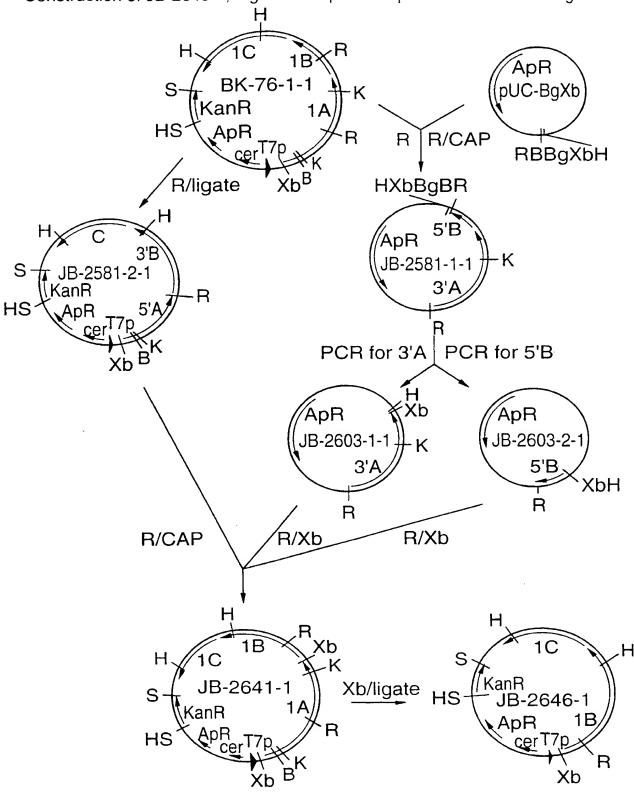
	15-2
EE	Joyc-1
NSKVAEV	Joyc-2
	LCDC2-1
sNERR.R.KE.EV	LCDC2-2
NSERR.R.KEV	PMH1-1
NSERR.R.KEV	PMH1-2
EE	K1-1
SSKVAEV	K21-1
1510 1520 1530	
LSRIVISEGRACFSNSDGATVCVNIADNGR-*	12-1
S.QVIKSGNRT.VD.QP*	12-2
S.QVTKSGNAT.VD.QQ*	15-1
S.QVTKVLIGNI.TIE.*	15-2
*	Joyc-1
S.QVTDKSGNAT.VT.DRQ*	Joyc-2
S.QVTKVLIGNI.TIE.*	LCDC2-1
S.QVTKSGNAT.VD.QQ*	LCDC2-2
S.QVIKSGNAT.VD.QP*	PMH1-1
S.QVIKSGNAT.VD.QP*	PMH1-2
QVTKVLIGNI.TIE*	K1-1
S.QVTKSGNAT.VD.QQ*	K21-1

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hmw2.				
nes were hawl or	SEO ID NO	75	76 77 78	79 80 81
amplified <i>hmw</i> A ge	5672.SL	5676.SL	5742.SL	5743.SL
whether PCR	3,	3,		
Oligonucleotides used to determine whether PCR amplified $hmA$ genes were $hmM$ or $hmM$ .	TCTTTTGCTGTGGCTGATGCCCCTA	CACTGATAGGTTGCTCATATTCGCC	V G V H K N GGTTGATGTTCATAAAATAT CCAACTACAAGTATTTTTATA 5'	G G S L T I N S GGCGGAAGTTTAACTATTAACTC CCGCCTTCAAATTGATAATTGAG 5'
Oliç	2,	5,	3,	3,

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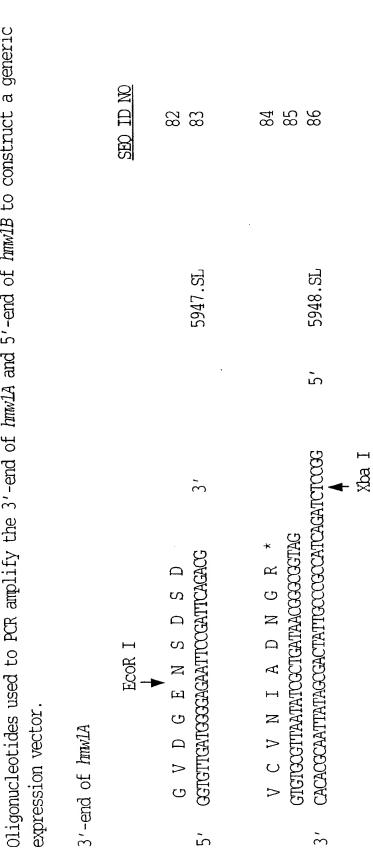
Construction of JB-2646-1, a generic expression plasmid for hmwABC genes



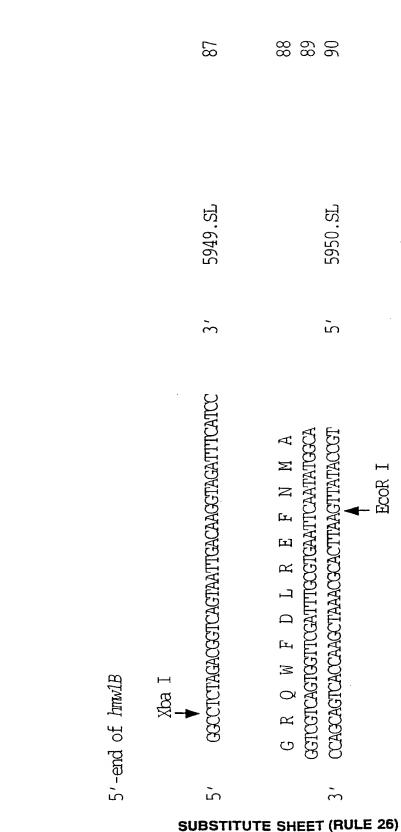
pT7 hmw1BC(12)/cer/KanR

FIG.32A

Oligonucleotides used to PCR amplify the 3'-end of hmwlA and 5'-end of hmwlB to construct a generic



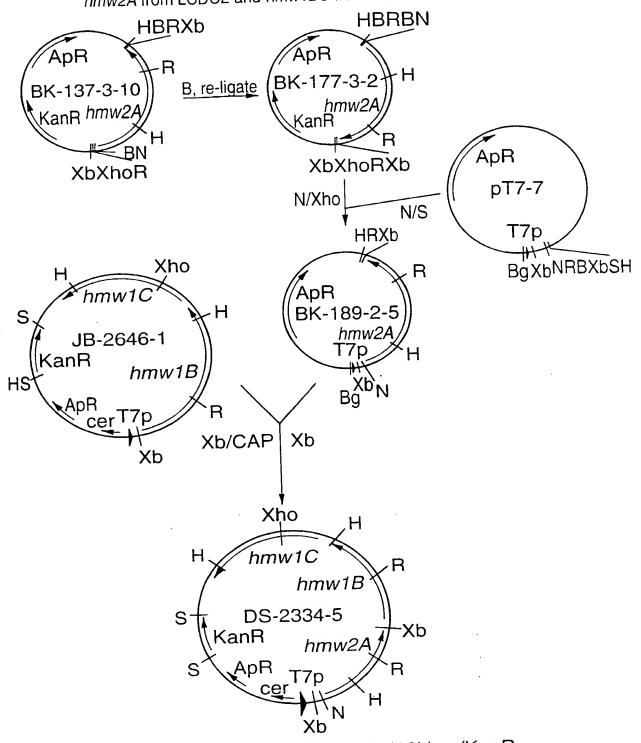
-1G.32B'



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Construction of DS-2334-5, a chimeric expression plasmid with hmw2A from LCDC2 and hmw1BC from strain 12



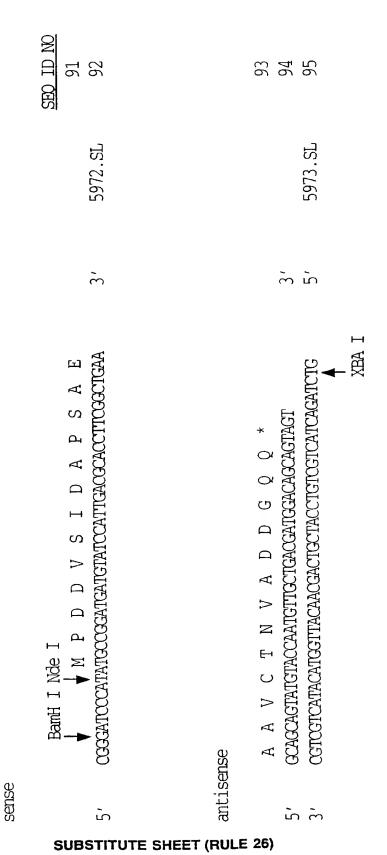
pT7hmw2A (LCDC2)/hmwBC (12)/cer/KanR

FIG.33A

Oligonucleotides used to PCR amplify the LCDC2 hmw2A gene for expression

FIG.33B

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Construction of DS-2400-13, a pBR T7 hmwA/T7 hmwABC/cer/KanRplasmid

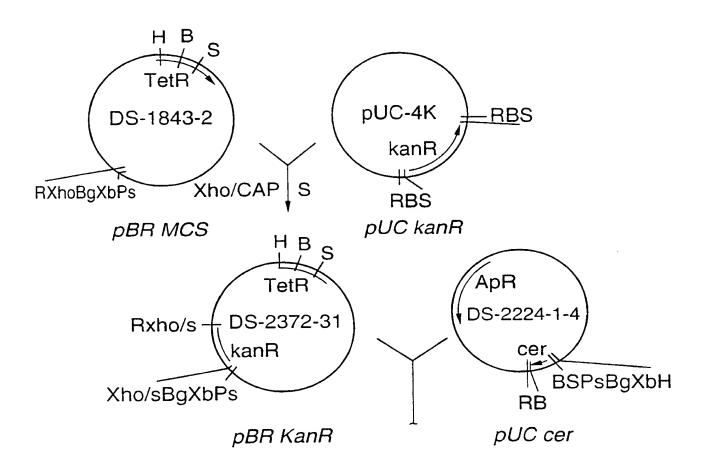
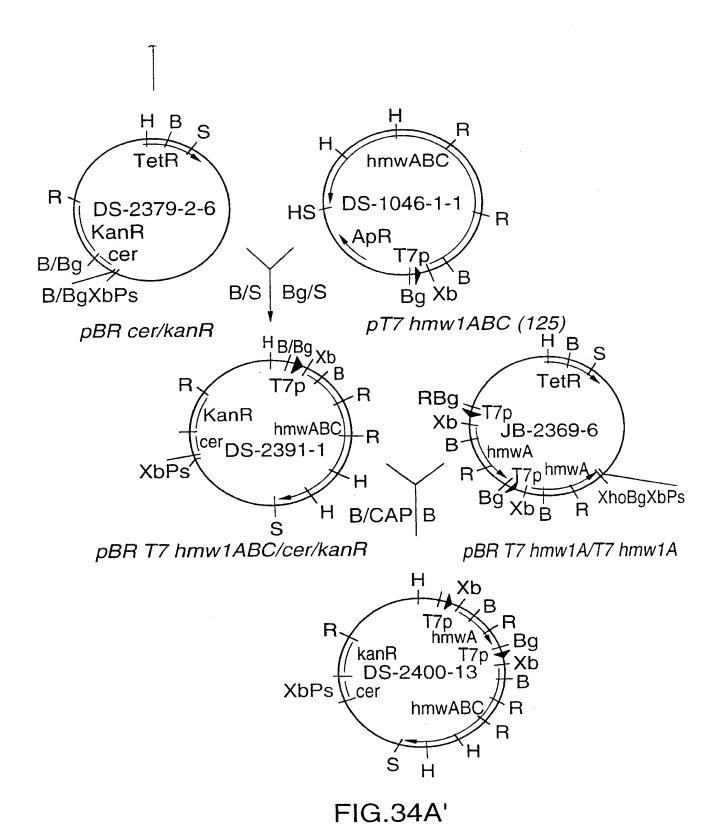


FIG.34A



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